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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 13.037 seconds
(without alignments)
41.218 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122
Sequence: 1 GPKGRNVLEKKWCAPTITNDG 22

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 231628 seqs, 24425594 residues

al number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued Patents_AA:*

1: /cgn2_6/pcodata/1/1aa/3A.COMB.pep:*
2: /cgn2_6/pcodata/1/1aa/3B.COMB.pep:*
3: /cgn2_6/pcodata/1/1aa/8A.COMB.pep:*
4: /cgn2_6/pcodata/1/1aa/8B.COMB.pep:*
5: /cgn2_6/pcodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/pcodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	100.0	215	2	US-08-997-080-117
2	122	100.0	215	2	US-08-997-362-117
3	122	100.0	215	4	US-09-095-855-117
4	122	100.0	215	4	US-09-324-542-117
5	122	100.0	523	2	US-08-997-080-114
6	122	100.0	523	2	US-08-997-362-114
7	122	100.0	523	4	US-09-095-855-114
8	122	100.0	523	4	US-09-324-542-114
9	122	100.0	540	2	US-08-368-834-20
10	122	100.0	540	4	US-08-461-722-3
11	122	100.0	540	4	US-08-461-722-4
12	122	100.0	540	4	US-08-336-251-3
13	122	100.0	540	4	US-08-336-251-4
14	122	100.0	540	5	PCIT-US94-06362-3
15	122	100.0	540	5	PCIT-US94-06362-4
16	122	100.0	541	2	US-08-467-822-34
17	122	100.0	541	2	US-08-447-154-19
18	122	100.0	541	2	US-08-997-080-160
19	122	100.0	541	2	US-08-997-362-160
20	122	100.0	541	4	US-09-095-855-160
21	122	100.0	541	4	US-08-432-697-34
22	122	100.0	541	4	US-08-466-248-34
23	122	100.0	541	4	US-09-324-542-160
24	98	80.3	547	4	US-08-461-722-2
25	98	80.3	547	4	US-08-336-251-2
26	98	80.3	547	5	PCIT-US94-06362-2
27	98	80.3	548	2	US-08-467-822-31

28	98	80.3	548	2	US-08-467-822-32	Sequence 32, App1
29	98	80.3	548	4	US-09-472-971-3	Sequence 3, App1
30	98	80.3	548	4	US-08-432-697-31	Sequence 31, App1
31	98	80.3	548	4	US-08-432-697-32	Sequence 32, App1
32	98	80.3	548	4	US-08-466-248-31	Sequence 31, App1
33	98	80.3	548	4	US-08-466-248-32	Sequence 32, App1
34	88	72.1	547	2	US-08-467-822-35	Sequence 35, App1
35	88	72.1	547	4	US-08-432-697-35	Sequence 35, App1
36	88	72.1	547	4	US-08-466-248-35	Sequence 35, App1
37	88	72.1	573	4	US-08-461-722-1	Sequence 1, App1
38	88	72.1	573	4	US-08-336-251-1	Sequence 1, App1
39	88	72.1	573	5	PCIT-US94-06362-1	Sequence 1, App1
40	87	71.3	545	2	US-08-467-822-30	Sequence 30, App1
41	87	71.3	545	4	US-08-432-697-30	Sequence 30, App1
42	87	71.3	545	4	US-08-466-248-30	Sequence 30, App1
43	87	71.3	546	3	US-08-470-260-6	Sequence 6, App1
44	87	71.3	546	3	US-08-471-491-6	Sequence 6, App1
45	87	71.3	546	4	US-08-466-662-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-08-997-080-117
; Sequence 117, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,080
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 117:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-997-080-117
Query Match 100.0%; Score 122; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWCAPTITNDG 22

Db 31 GPKGRNVLEKKWGAAPTINDG 52

RESULT 2

US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match

Best Local Similarity 100.0%; Score 122; DB 2; Length 215;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAAPTINDG 22

Db 31 GPKGRNVLEKKWGAAPTINDG 52

RESULT 3

US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Compounds and Methods for

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 29-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match

Best Local Similarity 100.0%; Score 122; DB 4; Length 215;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAAPTINDG 22

Db 31 GPKGRNVLEKKWGAAPTINDG 52

RESULT 4

US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 117

LENGTH: 215

TYPE: PRT

ORGANISM: Mycobacterium vaccae
US-09-324-542-117

Query Match 100.0%; Score 122; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 9e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAFTTNDG 22
DB 31 GPKGRNVLEKKWGAFTTNDG 52

RESULT 5
US-08-997-080-114

Sequence 114, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997.080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-114

Query Match 100.0%; Score 122; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAFTTNDG 22
DB 31 GPKGRNVLEKKWGAFTTNDG 52

RESULT 6
US-08-997-362-114

Sequence 114, Application US/08997362
Patent No. 5985287
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Miyama, Jun

APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 523 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-114

Query Match 100.0%; Score 122; DB 2; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAFTTNDG 22
DB 31 GPKGRNVLEKKWGAFTTNDG 52

RESULT 7
US-09-095-855-114

Sequence 114, Application US/09095855
Patent No. 6160093
GENERAL INFORMATION:
APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 28-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
;
; INFORMATION FOR SEQ ID NO: 114:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 523 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-095-855-114
Query Match 100.0%; Score 122; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
Db 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 8
US-09-324-542-114
; Sequence 114, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 114
; LENGTH: 523
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
US-09-324-542-114
Query Match 100.0%; Score 122; DB 4; Length 523;
Best Local Similarity 100.0%; Pred. No. 2.6e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
Db 31 GPKGRNVLEKKWGAPTTNDG 52
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; RESULT 9
US-08-368-834-20
; Sequence 20, Application US/08368834
; Patent No. 5874405
; GENERAL INFORMATION:
; APPLICANT: Birnbaum, Gary
; APPLICANT: Kotilinek, Linda K.
; APPLICANT: Braun, Peter E.
; TITLE OF INVENTION: Heat Shock Protein Peptides That Share
; TITLE OF INVENTION: Sequences with Cyclic Nucleotide Phosphodiesterase and
; TITLE OF INVENTION: Methods for Modulating Autoimmune Central Nervous System
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5874405west Center
; CITY: Minneapolis
; STATE: Minnesota
; COUNTRY: USA
; ZIP: 55402
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,834
; FILING DATE: 16-DEC-1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Katherine M.
; REGISTRATION NUMBER: 36,848
; REFERENCE/DOCKET NUMBER: 600.303US01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
;
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-368-834-20
Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
Db 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 10
US-08-461-722-3
; Sequence 3, Application US/08461722
; Patent No. 6335183
; GENERAL INFORMATION:
; APPLICANT: Young, Richard A. and Young, Douglas
; TITLE OF INVENTION: Stress Proteins and Uses Therefor
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: 2 Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FILING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-722-3

Query Match
Best Local Similarity 100.0%; Score 122; DB 4; Length 540;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GPKGRNVLEKKWGAPTTINDG 22
|||||
31 GPKGRNVLEKKWGAPTTINDG 52
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RESULT 11
US-08-461-722-4
Sequence 4, Application US/08461722
Patent No. 6335183
GENERAL INFORMATION:
APPLICANT: Young, Richard A. and Young, Douglas
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,722
FILING DATE: 05-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WHI88-08AFA4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-722-4

Query Match
Best Local Similarity 100.0%; Score 122; DB 4; Length 540;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPKGRNVLEKKWGAPTTINDG 22
|||||
Db 31 GPKGRNVLEKKWGAPTTINDG 52
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RESULT 12
US-08-336-251-3
Sequence 3, Application US/08336251
Patent No. 6338952
GENERAL INFORMATION:
APPLICANT: Young, Richard S.
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,251
```

FILED DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH188-08AFA3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-251-3

Query Match 100.0%; Score 122; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2,7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 13
US-08-336-251-4
Sequence 4, Application US/08336251
GENERAL INFORMATION:
APPLICANT: Young, Richard S.
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,251
FILING DATE: 03-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/804,632
FILING DATE: 09-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/366,581
FILING DATE: 15-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/207,298
FILING DATE: 15-JUN-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US89/02619
FILING DATE: 15-JUN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH188-08AFA3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-336-251-4

Query Match 100.0%; Score 122; DB 4; Length 540;
Best Local Similarity 100.0%; Pred. No. 2,7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTINDG 22
DB 31 GPKGRNVLEKKWGAPTINDG 52

RESULT 14
PCT-US94-06362-3
Sequence 3, Application PC/TUS9406362
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Stress Proteins and Uses Therefor
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: 2 Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06362
FILING DATE: 06-JUN-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,381
FILING DATE: 04-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: WH188-08AFA2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-06362-3

Query Match 100.0%; Score 122; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPPTINDG 22
|||||
DB 31 GPKGRNVLEKKWGAPPTINDG 52

RESULT 15

PCT-US94-06362-4

; Sequence 4, Application PC/TUS9406362

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Stress Proteins and Uses Therefor

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: 2 Miltia Drive

CITY: Lexington

STATE: MA

COUNTRY: USA

ZIP: 02173

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/06362

FILING DATE: 06-JUN-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/073,381

FILING DATE: 04-JUN-1993

ATTORNEY/AGENT INFORMATION:

NAME: Granahan, Patricia

REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: WH18-08AFA2 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 861-6240

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 540 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-06362-4

Query Match 100.0%; Score 122; DB 5; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.7e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPPTINDG 22
|||||
DB 31 GPKGRNVLEKKWGAPPTINDG 52

Search completed: October 17, 2002, 17:30:15
Job time : 14.037 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 ; Search time 30.963 Seconds
(without alignments)
78,921 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVVLEKKWCAPIITNDG 22

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	22	21	AAV93328
2	122	100.0	215	19	AAAM60145
3	122	100.0	215	20	AAV14892
4	122	100.0	295	22	AAAB3615
5	122	100.0	523	19	AAAM60144
6	122	100.0	523	20	AAV14891
7	122	100.0	539	20	AAV23919
8	122	100.0	540	9	AAAB1351
9	122	100.0	540	16	AAAB1610
10	122	100.0	540	18	AAW32100
11	122	100.0	540	19	AAW4702

12	122	100.0	540	20	AAV23911
13	122	100.0	540	21	AAV93332
14	122	100.0	540	22	AAE11755
15	122	100.0	540	22	AAAB1118
16	122	100.0	540	22	AAAB31606
17	122	100.0	541	16	AAAB67384
18	122	100.0	541	20	AAV14909
19	122	100.0	541	20	AAV23910
20	122	100.0	541	20	AAV23913
21	122	100.0	544	18	AAW32099
22	122	100.0	560	9	AAAB0215
23	122	100.0	572	11	AAAB04716
24	122	100.0	573	11	AAAB04715
25	122	100.0	573	16	AAAB64765
26	122	100.0	573	16	AAAB64766
27	122	100.0	588	9	AAAB0364
28	122	100.0	638	21	AAAB03790
29	122	100.0	639	22	AAAB31609
30	122	100.0	648	22	AAAB31614
31	122	100.0	948	22	AAAB31611
32	117	95.9	612	22	AAAB63908
33	116	95.1	548	17	AAAB94368
34	116	95.1	548	22	AAAG92732
35	111	91.0	95	22	AAU45697
36	107	87.7	440	13	AAAR22362
37	107	87.7	540	13	AAAR22363
38	103	84.4	52	13	AAAR20195
39	103	84.4	544	20	AAV23905
40	101	82.8	545	20	AAV23930
41	99	81.1	539	20	AAV23906
42	98	80.3	260	22	ABG24445
43	98	80.3	540	22	AAAM01101
44	98	80.3	541	20	AAV23802
45	98	80.3	544	20	AAV23903

ALIGNMENTS

RESULT 1
AAV93328 standard; peptide: 22 AA.
XX
XX
AC AAV93328;
XX
XX
DT 04-SEP-2000 (first entry)
XX
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW Inflammatory disorder; arthritis.
XX
XX
OS Mycobacterium tuberculosis.
XX
XX
PN WO200027870-A1.
XX
XX
PD 18-MAY-2000.
XX
XX
PF 04-NOV-1999; 99WO-IL00595.
XX
XX
PR 05-NOV-1998; 98US-0107213.
XX
XX
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
XX
XX
PI Naparstek Y, Ulanovsky R, Kasht Y;
XX
XX
DR WPI; 2000-376486/32.
XX
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT Immunity against autoimmune disease or inflammatory disorders,
PT especially arthritis -
XX
XX
PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of *Mycobacterium tuberculosis*. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.

XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 122; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.7e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTTNDG 22
 |||||
 DB 1 GPKGRNVLEKKWGAPTTNDG 22

PLT 2
 AAM60145 standard; Protein: 215 AA.

XX AAM60145;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27A sequence.

KW *Mycobacterium vaccae*; antigen; therapy; prevention; cytokine production;
 KM *M. avium*; *M. tuberculosis*; immune response enhancer; cell proliferation;
 KW *Mycobacteria* infection; vaccine; cancer.

XX *Mycobacterium vaccae*.

PN WO9608542-A2.

XX 05-MAR-1998.

PF 28-AUG-1997; 97WO-NZ00105.

PR 12-JUN-1997; 97US-0873970.

PR 29-AUG-1996; 96US-0703347.

XX (GENE-) GENESIS RES & DEV CORP.

PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

PT Visser E;

DR WPI: 1998-216926/19.

DR N-PSDB: AAV34609.

PT *Mycobacterium vaccae* polypeptides - used to develop products for use
 PT in detection, therapy and prevention of *Mycobacteria* infections or
 PT as immune response enhancers

PS Claim 48; Pages 117-118; 153pp; English.

XX This represents a *Mycobacterium vaccae* antigen GV-27A. The invention
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an
 CC immune response in patients previously exposed to a *Mycobacterium*. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by *Mycobacteria*
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.,
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
 CC B cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

XX Sequence 215 AA;

Query Match 100.0%; Score 122; DB 19; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPTTNDG 22
 |||||
 DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 3

AAY14892
 ID AAY14892 standard; protein: 215 AA.

XX AAY14892;

DT 25-OCT-1999 (first entry)

DE Amino acid sequence of M. vaccae antigen GV-27A.

XX *Mycobacterium vaccae* protein; antigen; T cell activation; cytokine;
 KW dendritic cell maturation; infectious disease; immune disorder; cancer;
 KW respiratory system; *Mycobacterial* infection; allergy; tuberculosis;
 KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;
 KW dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
 KW squamous cell carcinoma; melanoma.

XX *Mycobacterium vaccae*.

PN WO932634-A2.

XX 01-JUL-1999.

PF 23-DEC-1998; 98WO-NZ00189.

PR 04-DEC-1998; 98US-0205426.

PR 23-DEC-1997; 97US-0996824.

PR 23-DEC-1997; 97US-0997080.

PR 23-DEC-1997; 97US-0997362.

PR 11-JUN-1998; 98US-0095855.

PR 17-SEP-1998; 98US-0156181.

XX (GENE-) GENESIS RES & DEV CORP LTD.

PI Prestidge RL, Skinner MA, Tan P, Visser ES, Watson J;

PT WPI: 1999-430163/36.

DR N-PSDB: AAZ11344.

XX Enhancing immune response to an antigen

PS Example 14; Page 191-192; 243pp; English.

XX The invention provides heat-killed *Mycobacterium vaccae*, or recombinant
 CC M. vaccae proteins. The M. vaccae proteins may be employed to activate
 CC T cells and natural killer cells, to stimulate the production of
 CC cytokines, to enhance the expression of co-stimulatory molecules on
 CC dendritic cells and monocytes, and to enhance dendritic cell maturation
 CC and function. The proteins can be expressed by standard recombinant
 CC methodology. Pharmaceutical compositions comprising the proteins or
 CC nucleic acid sequences encoding the proteins can be used for the
 CC treatment, prevention, and detection of disorders including infectious
 CC diseases, immune disorders and cancer. In particular, the compounds and
 CC methods are used for treatment of diseases of the respiratory system,
 CC such as *Mycobacterial* infections, asthma, allergies, tuberculosis,
 CC leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
 CC psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
 CC alopecia areata, and skin cancers such as basal carcinoma, squamous cell
 CC carcinoma and melanoma.

XX Sequence 215 AA;

Query Match 100.0%; Score 122; DB 20; Length 215;
 Best Local Similarity 100.0%; Pred. No. 4.1e-12;

XX

KM Mycobacterium vaccae protein; antigen; T cell activation; cytokine;
KM dendritic cell maturation; infectious disease; immune disorder; cancer;

KW leprosy; sarcoidosis; lung cancer; asthma; skin disorder; psoriasis;

KW	dermatitis; eczema; alopecia areata; skin cancer; basal carcinoma;
KV	squamous cell carcinoma; melanoma.
XX	
OS	Mycobacterium vaccae.
PN	WO9932634-A2.
XX	
PD	01-JUL-1999.
XX	
PF	23-DEC-1998; 98WO-NZ00189.
XX	
PR	04-DEC-1998; 98US-0205426.
PR	23-DEC-1997; 97US-0996624.
PR	23-DEC-1997; 97US-0997080.
PR	23-DEC-1997; 97US-0997362.
PR	11-JUN-1998; 98US-0095855.
PR	17-SEP-1998; 98US-0156181.
XX	
PA	(GENE-) GENESIS RES & DEV CORP LTD.
XX	
DR	Prestidige RL, Skinner MA, Tan P, Visser ES, Watson J;
DR	WPI: 1999-430163/36.
XX	
DR	N-PSDB: AA211343.
XX	
PT	Enhancing immune response to an antigen
XX	
PS	Example 14; Page 189-190; 243pp; English.
XX	
CC	The invention provides heat-killed Mycobacterium vaccae, or recombinant
CC	M. vaccae proteins. The M. vaccae proteins may be employed to activate
CC	T cells and natural killer cells, to stimulate the production of
CC	cytokines, to enhance the expression of co-stimulatory molecules on
CC	dendritic cells and monocytes, and to enhance dendritic cell maturation
CC	and function. The proteins can be expressed by standard recombinant
CC	methodology. Pharmaceutical compositions comprising the proteins or
CC	nucleic acid sequences encoding the proteins can be used for the
CC	treatment, prevention, and detection of disorders including infectious
CC	diseases, immune disorders and cancer. In particular, the compounds and
CC	methods are used for treatment of diseases of the respiratory system,
CC	such as mycobacterial infections, asthma, allergies, tuberculosis,
CC	leprosy, sarcoidosis and lung cancers, and disorders of the skin such as
CC	psoriasis, atopic dermatitis, eczema, allergic contact dermatitis,
CC	alopecia areata, and skin cancers such as basal carcinoma, squamous cell
CC	carcinoma and melanoma.
XX	
SO	Sequence 523 AA;
XX	
QY	100.0%; Score 122; DB 20; Length 523;
DB	Test Local Similarity 100.0%; Pred. No. 1.2e-11;
XX	Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GPKGRNVLEKKMGAPTTINDG 22
DB	
XX	31 GPKGRNVLEKKMGAPTTINDG 52
XX	
RESULT 7	
AAAY23919	
ID	AAAY23919 standard; Protein; 539 AA.
XX	
XX	AAAY23919;
XX	
DT	22-SEP-1999 (first entry)
XX	
DE	Amino acid sequence of a heat shock protein.
XX	
KW	Heat shock protein; Hsp; immune response; immunological carrier;
KV	cancer control; tumour; sarcoma; cancer; gene therapy.
XX	
OS	Tsukamurella sp.
XX	
PN	WO9935270-A1

```

XX PD      15-JUL-1999.
XX PF      29-DEC-1998;   98WO-CA01203.
XX PR      31-DEC-1997;   97US-0001737.
XX PA      (STRE-) STRESSGEN BIOTECHNOLOGIES CORP.
XX PI      Mizzzen L, Wisniewski J;
XX DR      WPI; 1999-430397/36.
XX PT      New nucleic acid encoding heat shock protein-60 from Streptococcus,
XX PR      useful in vaccines, as carriers for other immunogens, as anticancer
XX PI      agents and for diagnosis
XX PS      Disclosure; Fig 10A-E; 176pp; English.
XX CC      AAY23905-30 represent heat shock proteins (Hsps). The specification
CC CC      describes Streptococcal Hsps, designated Hsp60. These proteins, their
CC CC      fragments, variants and fusion proteins, are used to elicit or enhance
CC CC      an immune response against Streptococcus, and to elicit a similar
CC CC      response to a target antigen fused to the protein. Unlike other
CC CC      immunological carriers, Hsp60 proteins are not immunosuppressive so
CC CC      provide an increased response to any conjugated or fused antigen. Also,
CC CC      where used for cancer control, they lack the side effects associated
CC CC      with endotoxins. They can also be used to detect specific antibodies
CC CC      and in treatment or prevention of tumours (e.g. sarcoma or cancers of
CC CC      breast, ovary, prostate, lung, pancreas or liver). The Hsp60
CC CC      polypeptide is used for recombinant production of the protein, as
CC CC      a source of primers and probes for detecting streptococci in standard
CC CC      hybridization/amplification assays, and therapeutically in gene
CC CC      therapy vectors.
XX SQ      Sequence      539 AA;

Query Match          100.0%; Score 122; DB 20; Length 539;
Best Local Similarity 100.0%; Pred. No. 1,2e-11;
Matches    22; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY      1 GPKGRNVYLEKKWGAPTTINDG 22
        |||||||
DB       31 GPKGRNVLEKKGWGAPTTINDG 52

RESULT 8
AAPB1351
ID AAPB1351 standard; protein; 540 AA.
XX AC      AAPB1351;
XX DT      29-DEC-1990 (first entry)
XX DE      Sequence of Mycobacterium tuberculosis 540 AA residue protein.
XX KM      Diagnosis: assay; M.bovis; vaccine.
XX OS      Mycobacterium tuberculosis.
XX PN      WO8806591-A.
XX PD      07-SEP-1988.
XX PF      25-FEB-1988;   88WO-US00598.
XX PR      24-FEB-1988;   88US-0159667.
XX PA      (SCRI-) SCRIPPS CLINIC & RE.
XX PI      Shinnick T, Houghten R;
XX DR      WPI; 1988-271136/38.
```


DR N-PSDB: AAN81768.
 XX Recombinant mycobacterial peptide(s) -
 PT used in assays for diagnosis of infection, for producing
 PT vaccines and for producing antibodies
 XX
 PS Disclosure: Fig 2a-2d; 116pp; English.
 XX
 CC An isolated DNA molecule that consists essentially of the nucleotide
 CC sequence that corresponds to the sequence represented by position 3950
 CC to about 2390 and from position 3948 through position 2398 of AAN81768
 CC is claimed. Also claimed is a peptide sequence that consists of a 5-40
 CC AA residue sequence that corresponds to a sequence of the 540 AA residue
 CC protein (AAP81351) or the 517 AA residue protein (AAP81868) coded for by
 CC the DNA sequence. The proteins can be used for determining previous
 CC immunological exposure of a mammal to M.tuberculosis or M.bovis and
 CC for producing a vaccine.
 XX
 SQ Sequence 540 AA;
 Query Match 100.0%; Score 122; DB 9; Length 540;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGAPTTNDG 22
 ID AAN81610 standard; protein: 540 AA.
 AC AAR81610;
 XX
 DT 09-MAY-1996 (first entry)
 XX
 DE Mycobacterium tuberculosis heat shock protein hsp65.
 XX
 KW Heat shock protein: mycobacterium tuberculosis; inflammatory disease;
 KW autoimmune disease: diabetes; arthritis; atherosclerosis; antibody;
 KW multiple sclerosis; myasthenia gravis; transplant rejection; diagnosis;
 KW therapy.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO9525744-A1.
 XX
 PF 28-SEP-1995.
 XX
 PR 21-MAR-1995; 95WO-NL00108.
 XX
 PR 10-OCT-1994; 94EP-0202927.
 XX
 PR 21-MAR-1994; 94EP-0200721.
 XX
 PR 22-MAR-1994; 94EP-0200738.
 XX
 PA (UYUT-) RIKSUNIV UTRECHT.
 XX
 PI Anderton SM, Van Der Zee R, Van Eden W;
 XX
 DR WPI: 1995-344587/44.
 XX
 PT Microbial stress protein fragments containing epitope(s) homologous
 PT to related mammalian epitope(s) - used to treat and prevent
 PT inflammation e.g. auto-immune diseases, also nucleic acids, vectors
 PT and recombinant cells
 XX
 PS Claim 4; Fig 13; 65pp; English.
 XX
 CC This sequence represents the heat shock protein hsp65 of Mycobacterium
 CC tuberculosis. The peptide fragments of this sequence represented by
 CC AAR81611-R81623 were used to immunise rat T-cells. These peptide
 CC fragments represent regions of stress proteins that are highly conserved

CC between microorganisms and animals. The immunisation was carried out in
 CC order to protect the rat from inflammatory diseases. The inflammatory
 CC diseases that the peptides can be used to treat include autoimmune
 CC diseases such as diabetes, arthritis, atherosclerosis, multiple sclerosis
 CC and myasthenia gravis. They also prevent transplant rejection.
 CC Antibodies raised against the peptide sequences can be used in diagnosis,
 CC e.g. to measure expression of the epitopes at sites of inflammation, or
 CC to measure T-cell proliferation or cytokine production. The antibodies
 CC can also be used for passive immunisation. The peptide fragments
 CC corresponding to similar regions of mammalian stress proteins do not
 CC elicit a protective response.
 XX
 SQ Sequence 540 AA;
 Query Match 100.0%; Score 122; DB 16; Length 540;
 Best Local Similarity 100.0%; Pred. No. 1.2e-11;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPKGRNVLEKKWGAPTTNDG 22
 ID AAW32100 standard; protein: 540 AA.
 AC AAW32100;
 XX
 DT 08-APR-1998 (first entry)
 XX
 DE Mycobacteria sp. heat shock protein 65 (hsp65) #2.
 XX
 KW Heat shock protein: hsp65; human; autoimmune disease: hsp65;
 KW rheumatoid arthritis; antigen; infectious disease: prophylactic;
 KW pristanic induced arthritis; PIA; vaccine.
 XX
 OS Mycobacteria sp.
 XX
 PN WO9711966-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 XX
 DR WPI: 1997-212851/19.
 XX
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 PT for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure: Fig 4; 91pp; English.
 XX
 CC This is the heat shock protein hsp65 which can be used in a novel method
 CC to treat autoimmune disease e.g. rheumatoid arthritis. This sequence is
 CC known to be an immunodominant antigen in a number of infectious diseases
 CC and is linked to pristanic induced arthritis (PIA) in vitro. HSP's from
 CC microbial sources may act as self antigens and thus have limited use
 CC whereas the human hsp65 homologue, hsp68 or fragments of the hsp68
 CC protein may be useful in the development of vaccines for prophylaxis or
 CC treatment of an autoimmune disease such as rheumatoid arthritis.
 CC Note: this hsp65 sequence is represented in Figure 4 but differs
 CC slightly from the hsp65 sequence given in the sequence specification (see
 CC AAW32099).
 XX
 SQ Sequence 540 AA;
 Query Match 100.0%; Score 122; DB 18; Length 540;

XX 04-SEP-2000 (first entry)
DT
XX
DE Amino acid sequence of a heat shock protein 60.
XX
XX Eptlope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KM inflammatory disorder; arthritis.
XX
XX Mycobacterium tuberculosis.
OS
XX WO200027870-A1.
PN
XX
XX 18-MAY-2000.
PD
XX
XX 04-NOV-1999; 99WO-IL00595.
PF
XX
XX 05-NOV-1998; 98US-0107213.
PR
XX
XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
PA
Naparstek Y, Ulanovsky R, Kasht Y;
WPI; 2000-376486/32.
DR
XX Peptide having a defined sequence is used in vaccines for conferring
PT immunity against autoimmune disease or inflammatory disorders,
PR especially arthritis -
PS
XX Disclosure: Fig 1; 58pp; English.
PS
XX The present sequence represents a heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The specification
CC describes epitopes of Hsp60 proteins, which are useful in
CC vaccines for conferring immunity against autoimmune disease
CC or inflammatory disorders, especially arthritis. The peptide
CC may also be used to raise antibodies, which are then used for
CC passive immunisation.
CC
XX
SQ Sequence 540 AA:
Query Match 100.0%; Score 122; DB 21; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52
30LT 14
AE11755
ID AE11755 standard; Protein: 540 AA.
AC
XX
XX AE11755;
AC
XX
DT 18-DEC-2001 (first entry)
DT
XX
DE Mycobacterium tuberculosis heat shock protein 65 (HSP65).
XX
XX Heat shock protein 65; HSP65; antiatherosclerotic; antiinflammatory;
KM antiallergic; immunomodulator; dermatological; immunosuppressive;
KM vasoactive; immunostimulant; therapy; vascular disorder; immune response;
KM atherosclerosis; allergic angitis; Behcet's syndrome; granulomatosis;
KM Churg-Straus disease; Cogan's syndrome; graft-versus-host disease; GVHD;
KM Henoch-Schönlein purpura; leucocytoclastic vasculitis; Kawasaki disease;
KM polyarteritis nodosa; PAN; Takayasu's arteritis; temporal arteritis;
KM thrombocytopenic purpura; Wegener's disease; transplant rejection;
KM microscopic polyangitis.
XX
XX Mycobacterium tuberculosis.
OS
XX WO200168124-A2.
PN

XX 20-SEP-2001.
PD
XX
XX 15-MAR-2001; 2001WO-US08351.
PF
XX
XX 15-MAR-2000; 2000US-189855P.
PR
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
PA
XX
XX Welner HL, Maron R, Libby P;
PI
XX
XX WPI; 2001-611383/70.
DR
XX
XX
XX Treating a vascular disorder, involves administering a composition
PT comprising heat shock protein, its fragment or analog, by mucosal
PT surface, pulmonary tract, oral or enteral route, or by inhalation -
PR
XX
XX Disclosure: Page 11; 49pp; English.
PS
XX
XX The patent discloses methods for treating vascular disorders in
CC mammals. The method involves administering a composition comprising
CC at least one agent selected from heat shock protein (HSP), its fragment
CC or analogue, through mucosal surface, pulmonary tract, oral or enteral
CC route or by inhalation. Compositions comprising HSP are useful for
CC treating and suppressing a vascular disorder, including cell-mediated
CC immune response, an antibody-mediated immune response, cell-mediated
CC inflammatory disorder, atherosclerosis, allergic angitis, Behcet's
CC syndrome, granulomatosis (Churg-Straus disease), Cogan's syndrome,
CC graft-versus-host disease (GVHD), Henoch-Schönlein purpura, Kawasaki
CC disease, leucocytoclastic vasculitis, polyarteritis nodosa (PAN),
CC microscopic polyangitis, polyangitis overlap syndrome, Takayasu's
CC arteritis, temporal arteritis, transplant rejection, Wegener's
CC granulomatosis and thromboangitis obliterans (Buerger's disease).
CC They are useful for reducing the level of proinflammatory Th1 cytokines
CC and also for increasing the level of antiinflammatory Th2 cytokines.
CC The present sequence is heat shock protein 65 (HSP65) from
CC Mycobacterium tuberculosis.
CC
XX
SQ Sequence 540 AA:
Query Match 100.0%; Score 122; DB 22; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.2e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKKGAPTTNDG 22
DB 31 GPKGRNVLEKKKGAPTTNDG 52
RESULT 15
AAG81118
ID AAG81118 standard; Protein: 540 AA.
AC
XX
XX AAG81118;
AC
XX
DT 04-SEP-2001 (first entry)
DT
XX
DE Mycobacterium tuberculosis potential drug target protein SEQ ID 169.
XX
XX Drug target; growth; organism viability; characterisation.
KM
XX Mycobacterium tuberculosis.
OS
XX WO200135317-A1.
PN
XX
XX 17-MAY-2001.
PD
XX
XX 13-NOV-2000; 2000WO-US31152.
PF
XX
XX 12-NOV-1999; 99US-0165086.
PR 12-NOV-1999; 99US-0165124.
PR 01-FEB-2000; 2000US-0179531.
XX

PA (REGC) UNIV CALIFORNIA.

XX Eisenberg D, Rotstein SH, Marcotte EM;

XX WPI: 2001-329193/34.

DR N-PSDB: AAH51969.

XX Identifying nucleotide or polypeptide sequence for use as drug target,
PT involves providing algorithm that analyzes a functional relationship
PT between nucleotide or polypeptide sequences, and comparing the
PT sequences -

PS Disclosure: Page 160; 207pp; English.

XX This invention relates to a method for identifying a nucleotide or
CC polypeptide sequence that may be a drug target, or essential for growth
CC or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
CC represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium
CC tuberculosis proteins which are potential drug targets. The DNA and
CC protein sequences are used to illustrate the method of the invention. The
CC method involves providing an unknown nucleotide or polypeptide sequences,
CC and comparing it to a number of sequences along with at least one
CC algorithm capable of analysing a functional relationship between
CC nucleotide and polypeptide sequences. The method is useful for
CC characterising the function of nucleic acids and polypeptides that may be
CC useful as a target for a drug or essential for the growth or viability of
CC an organism.

XX Sequence 540 AA:

Query Match 100.0%; Score 122; DB 22; Length 540;

Best Local Similarity 100.0%; Pred. No. 1.2e-11;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKRWGAPTITNDG 22

|||||

Db 31 GPKGRNVLEKKRWGAPTITNDG 52

Search completed: October 17, 2002, 17:27:23
Job time : 32.963 secs

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 14.6667 Seconds
(without alignments)
144.134 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKWGAPITINDG 22

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

PIR_71: *
1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	540	2 A26950	groEL2 protein - M
2	122	100.0	540	2 A43509	65K antigen mbaa -
3	122	100.0	540	2 C41325	heat shock protein
4	122	100.0	541	2 S40245	heat shock protein
5	122	100.0	541	2 T44725	chaperonin 60K (im
6	122	100.0	588	2 A25902	65K antigen - Myco
7	112	91.8	538	2 H72367	groEL protein - Th
8	107	87.7	540	2 B41325	heat shock protein
9	107	87.7	541	2 T35591	chaperonin cpn60 -
10	103	84.4	538	2 J01195	heat shock protein
11	103	84.4	539	2 B49855	heat shock protein
12	103	84.4	541	2 S72614	chaperonin 60 - Th
13	103	84.4	542	2 AC1704	class I heat-shock
14	103	84.4	542	2 AD1333	class I heat-shock
15	103	84.4	543	2 B41872	heat shock protein
16	103	84.4	543	2 F97232	chaperonin groEL,
17	103	84.4	544	2 JC5130	heat shock protein
18	103	84.4	544	2 B41884	58K heat shock pro
19	103	84.4	544	2 JC6063	chaperonin groEL -
20	103	84.4	544	2 B83720	class I heat-shock
21	102	83.6	543	2 S70013	chaperonin-like pr
22	101	82.8	528	2 S73270	chaperonin, 60K -
23	101	82.8	541	2 T06829	chaperonin groEL -
24	101	82.8	544	2 AG2263	chaperonin groEL -
25	101	82.8	546	2 S34938	heat shock protein
26	100	82.0	541	2 S68249	chaperonin groEL h
27	100	82.0	544	1 BVCYGL	chaperonin groEL -
28	100	82.0	546	2 B47073	chaperonin groEL -
29	99	81.1	539	2 S22342	chaperonin HSP60 -

30	99	81.1	542	2 JN0661	heat shock protein
31	99	81.1	542	2 S32106	groEL protein - La
32	99	81.1	542	2 B86674	60 kD chaperonin I
33	98	80.3	540	2 G95222	chaperonin, 60 kDa
34	98	80.3	540	2 H98086	chaperonin groEL I
35	98	80.3	544	2 B82048	chaperonin, 60 kD
36	98	80.3	547	2 JC4519	heat shock protein
37	98	80.3	547	2 B43606	heat shock protein
38	98	80.3	547	2 B83098	groEL protein PA43
39	98	80.3	548	1 BVEGGL	chaperonin groEL -
40	98	80.3	548	2 D91269	chaperonin groEL I
41	98	80.3	548	2 G75499	groEL protein - De
42	98	80.3	548	2 B86110	hypothetical prote
43	98	80.3	548	2 AE1045	groEL protein (imp
44	98	80.3	550	2 A41468	60K heat shock pro
45	98	80.3	552	2 S39765	chaperonin 60 - Co

ALIGNMENTS

```
RESULT 1
A26950      groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C>Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A:Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; MUID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SHI>
R:Colle, S.T.; Brosch, R.; Parhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd,
Rajandream, M.A.; Rogers, J.; Ruter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete gene
A:Reference number: A70500; MUID:98295987
A:Accession: A70830
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-540 <COL>
A:Cross-references: GB:AL021932; GB:AL123456; MUID:93261527; PIDN:CAA17397.1; PID:9290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; RV0440
C:Superfamily: chaperonin groEL

Query Match      100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAPITINDG 22
Db 31 GPKGRNVLEKKWGAPITINDG 52

RESULT 2
A43509      65K antigen mbaa - Mycobacterium bovis
C:Species: Mycobacterium bovis
C>Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Bervald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A:Title: Characterization, sequence determination, and immunogenicity of a 64-kilodalton
A:Reference number: A43509; MUID:87193155
A:Accession: A43509
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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
|||||
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 3

CA1325
heat shock protein 56 - Streptomyces albus
N:Alternate names: heat shock protein groEL homolog 2
C:Species: Streptomyces albus
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999
C:Accession: CA1325

R:Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.
J. Bacteriol. 173, 7382-7386, 1991
A:Title: Characterization of the groEL-like genes in Streptomyces albus.
A:Reference number: A41325; MUID:92041639

A:Accession: CA1325
A:Molecule type: DNA
A:Residues: 1-540 <MAZ>
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294
C:Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
|||||
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 4

S40245
heat shock protein 65 - Mycobacterium paratuberculosis
C:Species: Mycobacterium paratuberculosis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S40245

R:Liston, X.Y.Z.; McConnell, X.Y.Z.; Bujdoso, R.
submitted to the EMBL Data Library, August 1993
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.
A:Reference number: S40245

A:Accession: S40245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <COL>
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
|||||
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 5

T44725
Chaperonin 60k [imported] - Mycobacterium leprae
N:Alternate names: heat shock protein groEL-2

C:Species: Mycobacterium leprae
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44725
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z22831

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Accession: T44725
A:Molecule type: DNA
A:Residues: 1-541 <JAM>

A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1
A:Experimental source: cosmid B1450

A:Gene: groEL-2
C:Superfamily: chaperonin groEL
C:Keywords: molecular chaperone

Query Match 100.0%; Score 122; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 9.5e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
|||||
DB 31 GPKGRNVLEKKKGAPTTNDG 52

RESULT 6

A25902
65k antigen - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997
C:Accession: A25902

R:Mehta, V.; Sweetser, D.; Young, R.A.
Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986
A:Title: Efficient mapping of protein antigenic determinants.
A:Reference number: A25902; MUID:86313701

A:Accession: A25902
A:Molecule type: DNA
A:Residues: 1-588 <MEH>
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 122; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 1e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKKGAPTTNDG 22
|||||
DB 78 GPKGRNVLEKKKGAPTTNDG 99

RESULT 7

H72367
groEL protein - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72367

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316

A:Accession: H72367
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <ARN>
A:Cross-references: GB:AE00127; GB:AE000512; NID:g4981015; PIDN:AA035591.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0506
C:Superfamily: chaperonin groEL

Query Match 91.8%; Score 112; DB 2; Length 538;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 7.74074 Seconds
(without alignments)
110.045 Million cell updates/sec

Title: US-09-847-637b-1
Perfect score: 122

Sequence: 1 GPKGRNVLEKKMGAPTITNDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Minimum number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Database : SWISSPROT_40.*
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	122	100.0	476	1 CH62_STRLI	O33658 streptomyc
2	122	100.0	539	1 CH62_MYCTU	P06806 mycobacteri
3	122	100.0	539	1 CH62_STRAL	O00768 streptomyc
4	122	100.0	540	1 CH60_MYCPA	P42384 mycobacteri
5	122	100.0	540	1 CH62_MYCLE	P09239 mycobacteri
6	112	91.8	538	1 CH60_THEMA	O3WY26 thermotoga
7	107	87.7	539	1 CH61_STRAL	O00767 streptomyc
8	107	87.7	540	1 CH61_STRCO	P40171 streptomyc
9	103	84.4	538	1 CH60_BACPC	P26209 bacillus ps
10	103	84.4	539	1 CH60_BACST	O07201 bacillus st
11	103	84.4	540	1 CH60_THEBR	O60024 thermoaer
12	103	84.4	543	1 CH60_BACSU	P28598 bacillus su
13	103	84.4	543	1 CH60_CLOAB	P30717 clostridium
14	103	83.6	544	1 CH60_BACHD	O50305 bacillus ha
15	102	83.6	543	1 CH62_SYNVU	O57002 synechococ
16	101	82.8	528	1 CH60_PORPU	P51349 porphyra pu
17	101	82.8	541	1 CH60_CVAPA	O27757 cyanophora
18	101	82.8	544	1 CH61_STINW	O50323 synechococ
19	101	82.8	546	1 CH60_LEPIN	P35468 leptospira
20	101	82.8	552	1 CH60_PSEST	O33500 pseudomonas
21	100	82.0	300	1 CH60_SYNP6	P12834 synechococ
22	100	82.0	540	1 CH60_CLOTM	P48212 clostridium
23	100	82.0	542	1 CH60_THERH	P45746 thermus agu
24	100	82.0	544	1 CH60_STNP7	P22879 synechococ
25	100	82.0	546	1 CH60_CHRW1	P31293 chromatiu
26	99	81.1	529	1 CH60_GUTTH	O78419 guillardia
27	99	81.1	539	1 CH60_CLOPE	P26821 clostridium
28	99	81.1	542	1 CH60_IACIA	P37282 lactococcus
29	98	80.3	539	1 CH60_ENTAG	O66200 enterobacte
30	98	80.3	539	1 CH60_ENTAM	O66196 enterobacte
31	98	80.3	539	1 CH60_ENTAS	O66190 enterobacte
32	98	80.3	539	1 CH60_ENTIT	O66192 enterobacte
33	98	80.3	539	1 CH60_SERRU	O66202 serratia ru

34	98	80.3	540	1 CH60_ENTAE	O66198 enterobacte
35	98	80.3	540	1 CH60_ENTGE	O66194 enterobacte
36	98	80.3	540	1 CH60_ERMAP	O66222 erwinia aph
37	98	80.3	540	1 CH60_ERMCA	O66220 erwinia car
38	98	80.3	540	1 CH60_KLEON	O66214 klebsiella
39	98	80.3	540	1 CH60_KLEOX	O66210 klebsiella
40	98	80.3	540	1 CH60_KLEPL	O66212 klebsiella
41	98	80.3	540	1 CH60_SERFI	O66204 serratia fi
42	98	80.3	540	1 CH60_SERMA	O66206 serratia ma
43	98	80.3	541	1 CH60_CERWE	O66216 erwinia her
44	98	80.3	541	1 CH60_PANAN	O66218 pantoea ana
45	98	80.3	544	1 CH60_AERSA	O68309 aeromonas s

ALIGNMENTS

RESULT 1	ID	CH62_STRLI	STANDARD:	PRT:	476 AA.
AC	O33658:				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	16-OCT-2001 (Rel. 40, Last annotation update)				
DE	60 kDa Chaparonin 2 (Protein Cpn60 2) (GroEL2 protein).				
GN	GROEL2 OR GROEL2.				
OS	Streptomyces lividans.				
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;				
OC	Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.				
OX	NCBI_TaxID=1916;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=TK21;				
RA	MEDLINE=98048481; Pubmed=9387235;				
RA	de Leon P., Marco S., Islegas C., Marina A., Carrascosa J.L.,				
RA	Mellado R.P.;				
RT	"Streptomyces lividans groEL, groEL1 and groEL2 genes."				
RL	Microbiology 143:3563-3571(1997).				
CC	-1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND				
CC	PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS				
CC	CONDITIONS (BY SIMILARITY).				
CC	-1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF				
CC	7 SUBUNITS (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL: X95971; CAA65226.1; -				
DR	HSSP: P45746; ISRV.				
DR	InterPro: IPR001844; Chaperonins_cpn60.				
DR	InterPro: IPR002423; TCPL_cpn60.				
DR	Pfam: PF00118; cpn60_Tcpl.1.				
DR	PRINTS: PR00298; CHAPERONIN60.				
DR	PRINTS: PR00304; TCOMPLEXTCP1.				
DR	PROSITE: PS00296; CHAPERONINS_CPN60.1.				
KW	Chaperone; ATP-binding; Multigene family;				
FT	INT-MET 0 BY SIMILARITY				
SO	SEQUENCE 476 AA; 50529 MW; 760F81793F4EDAD CRC64;				
Query Match	100.0%; Score 122; DB 1; Length 476;				
Best Local Similarity	100.0%; Pred. No. 2, 2e-10;				
Matches	22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
OY	1 GPKGRNVLEKKMGAPTITNDG 22				
DB	30 GPKGRNVLEKKMGAPTITNDG 51				

RESULT 2
CH62_MYCTU STANDARD; PRT; 539 AA.
ID CH62_MYCTU
AC P06806; Q48931; Q48920;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (Heat shock protein 65) (cell wall protein A) (Antigen A).
GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_Taxid=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=ERDMANN;
MEDLINE=87137260; PubMed=3029018;
Shinnick T.M.;
"The 65-kilodalton antigen of Mycobacterium tuberculosis.";
J. Bacteriol. 169:1080-1088(1987).
RL [2]
RN SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
MEDLINE=98295987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kirogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
RL [3]
RN SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Feldman J., Khouri H., Gill J., Mikula A., Bishai W.;
"Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains";
Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=BCG;
MEDLINE=87193155; PubMed=3553003;
Thole J.E.R., Keulen W.J., Kolk A.H.J., Grootuis D.G., Berwald L.G., Tiesema R.H., van Embden J.D.A.;
"Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of Mycobacterium bovis BCG expressed in Escherichia coli K-12.";
Infect. Immun. 55:1466-1475(1987).
RL [5]
RP SEQUENCE OF 45-195 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;
Ros C., Belak K.;
Submitted (May-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 63-182 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMC1024;
MEDLINE=95150784; PubMed=7848059;
Kaput V., Li L.L., Hamrick M.R., Plikaytis B.B., Shinnick T.M., Telenti A., Jacobs M.R. Jr., Banerjee A., Cole S., Yuen K.Y., Claridge J.E., Kreiswirth B.N., Musser J.M.;
"Rapid Mycobacterium species assignment and unambiguous identification of mutations associated with antimicrobial resistance

RT in Mycobacterium tuberculosis by automated DNA sequencing.";
Arch. Pathol. Lab. Med. 119:131-138(1995).
RN [7]
RP SEQUENCE OF 64-177 FROM N.A.
RC SPECIES=M.tuberculosis;
RX MEDLINE=95214306; PubMed=7699930;
RA Hidaka E., Ueno I., Kawakami Y., Furuwatari C., Furihata K., Katsuyama T.;
RT "Detection and identification of mycobacteria by PCR-RFLP method.";
J. Clin. Microbiol. 33:155-161(1995).
RL Rinsbo Hjort 43:155-161(1995).
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
CC -1- MISCELLANEOUS: PURIFIED 65 kDa ANTIGEN CAN ELICIT A STRONG DELAYED-TYPE HYPERSENSITIVITY REACTION IN EXPERIMENTAL ANIMALS INFECTED WITH M.TUBERCULOSIS. THIS PROTEIN IS ONE OF THE MAJOR IMMUNOREACTIVE PROTEINS OF THE MYCOBACTERIA. THIS ANTIGEN CONTAINS EPITOPES THAT ARE COMMON TO VARIOUS SPECIES OF MYCOBACTERIA.
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -----
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CC -----
DR EMBL; M15467; AAA8232.1; -;
DR EMBL; AL021932; CAI1797.1; -;
DR EMBL; AE006948; AAK44679.1; -;
DR EMBL; M17705; AAA25358.1; -;
DR EMBL; U55833; AAC44451.1; -;
DR EMBL; U55825; AAC44458.1; -;
DR EMBL; U17925; AAB39044.1; -;
DR EMBL; U17957; AAB39076.1; -;
DR EMBL; S76635; -; NOT_ANNOTATED_CDS.
DR PIR; A26950; A26950.
DR PIR; A43509; A43509.
DR HSSP; P45746; ISRV.
DR TIGR; MT0456; -;
DR TuberculList; RV0440; -;
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCP1_cpn60.
DR Pfam: PF00118; cpn60_TCP1.1.
DR PRINTS; PR00296; CHAPERONIN60.
DR PROSITE; PS00304; TCOMPLEXTCP1.
DR Chaperone; ATP-binding; CHAPERONINS_CPN60; 1.
KW Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
SQ SEQUENCE 539 AA; 56595 MW; FF03460BAA2BC557 CRC64;
Query Match 100.0%; Score 122; DB 1; Length 539;
Best local Similarity 100.0%; Pred. No. 2,4e-10;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAPlTNDG 22
DB 30 GPKGRNVLEKKWGAPlTNDG 51
ID CH62_STRAL STANDARD; PRT; 539 AA.
AC Q00768;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (protein Cpn60 2) (groEL protein 2) (HSP56).
GN GROEL2 OR GROEL2.

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 24.8519 Seconds
(without alignments)
153.143 Million cell updates/sec

Title: US-09-847-637B-1
Perfect score: 122
Sequence: 1 GPKGRNVLEKKWGAPRTINDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mmc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.todent:*
- 12: sp.virus:*
- 13: sp.vertibrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	100.0	59	2	Q9EMD1 streptomyc
2	122	100.0	61	2	Q9EUR7 streptomyc
3	122	100.0	539	2	P97086 tsukamurell
4	122	100.0	540	2	Q9AFAS tsukamurell
5	122	100.0	541	2	Q9KFW1 mycobacteri
6	122	100.0	541	2	Q9AFAS mycobacteri
7	122	100.0	541	2	Q9KXU5 streptomyc
8	122	100.0	541	2	Q9S0T2 corynebacte
9	122	100.0	542	2	Q9AFCS nocardia as
10	117	95.9	533	2	Q9FDS2 propionibac
11	117	95.9	544	2	Q9K2U4 propionibac
12	112	91.8	538	2	Q9EZV1 thermotoga
13	105	86.1	537	2	Q9K171 bifidobacte
14	105	86.1	541	2	Q9K157 bifidobacte
15	104	85.2	537	2	Q93M78 bifidobacte
16	104	85.2	582	2	Q9REU4 bifidobacte

17	103	84.4	539	2	Q9RC20 bacillus sp
18	103	84.4	539	2	Q9EZV4 bacillus st
19	103	84.4	542	2	Q9AGE6 listeria mo
20	103	84.4	542	16	Q929V0 listeria in
21	102	83.6	540	2	Q9XCA9 rhodothermu
22	102	83.6	543	2	Q9KJ23 lactobacillu
23	102	83.6	543	2	Q9AMJ8 anabaena sp
24	101	82.8	538	2	Q9EY76 bifidobacte
25	101	82.8	546	2	Q31198 leptospira
26	99	81.1	540	2	Q9KRF0 clostridium
27	99	81.1	540	2	Q9KJY7 clostridium
28	99	81.1	542	2	Q9AEP7 lactococcus
29	99	81.1	544	2	Q9XG73 bacteroides
30	98	80.3	82	2	Q9F4E5 buchnera ap
31	98	80.3	329	2	Q9ETC4 serratia ma
32	98	80.3	329	2	Q9EMB0 serratia ma
33	98	80.3	329	2	Q9EMW9 serratia ma
34	98	80.3	329	2	Q9EMW8 serratia ma
35	98	80.3	329	2	Q9F2H2 serratia ma
36	98	80.3	329	2	Q9EXM7 enterobacte
37	98	80.3	329	2	Q9EXM5 enterobacte
38	98	80.3	540	16	Q97NV4 streptococ
39	98	80.3	541	2	Q93EB6 enterococcu
40	98	80.3	544	16	Q9KNR7 vibrio chol
41	98	80.3	545	2	Q93F08 enterobacte
42	98	80.3	547	2	Q9ALA9 vibrio vuln
43	98	80.3	548	2	Q9L7P5 vibrio para
44	98	80.3	548	16	Q9RW09 delinococcu
45	97	79.5	524	10	Q49314 arabidopsis

ALIGNMENTS

RESULT 1									
ID	Q9EMD1	PRELIMINARY:	PRT:	59	AA.				
AC	Q9EMD1:								
DT	01-MAR-2001 (TREMBLrel. 16, Created)								
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)								
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)								
DE	HEAT-SHOCK PROTEIN (FRAGMENT).								
GN	GROEL2.								
OS	Streptomyces coelicolor.								
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;								
OC	Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.								
OX	NCBI_TaxID=1902;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=J802;								
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;								
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces								
RT	antibiotic biosynthesis."								
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.								
DR	EMBL: AJ250536; CAC19351.1; -.								
DR	HSSP: P06139; IAO.								
DR	InterPro: IPR002423; TCPI_cp060.								
DR	Pfam: PF00118; cp060_TCPI_1.								
DR	PRINTS: PR00304; TCOMPLEXTCP1.								
KW	ATP-binding; Chaperone.								
FT	NON_TER	59							
SO	SEQUENCE	59	AA;	6407	MW;	E7B24199B7DE68FA	CRC64;		
Query Match									
Best Local Similarity		100.0%;	Score 122;	DB 2;	Length 59;				
Matches 22; Conservativity		100.0%;	Pred. No. 8.8e-12;						
Mismatches		0;	Mismatches	0;	Indels	0;	Gaps	0;	
QY	1 GPKGRNVLEKKWGAPRTINDG 22								
DB	31 GPKGRNVLEKKWGAPRTINDG 52								
RESULT 2									

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Q9EUR7
ID Q9EUR7 PRELIMINARY; PRT; 61 AA.
AC Q9EUR7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetaceae; Streptomyces.
NCBI_Taxid=1912;

RM
RN
RP SEQUENCE FROM N.A.
RC STRAIN-AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RL antibiotic biosynthesis.";
RL Submitted (Oct-1999) to the EMBL/GenBank/DBJ databases.
EMBL; AJ250537; CAC19355.1; -.
HSSP; P06139; IACN.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR ATP-binding; Chaperone.
KW NON_TER
FT SEQUENCE 61 AA; 6645 MW; D200955F4199B7CA CRC64;

Query Match 100.0%; Score 122; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 9, 1e-12;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 3
P97086 PRELIMINARY; PRT; 539 AA.
AC P97086;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Tsukamurellaceae; Tsukamurella.
NCBI_Taxid=57704;

RM
RN
RP SEQUENCE FROM N.A.
RC STRAIN-IMMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
RL protein 60.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR Pfam; PF00118; cpn60_TCPL_1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 539 AA; 56137 MW; 6353514830C9B662 CRC64;

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Query Match 100.0%; Score 122; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 9e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 4
Q9AFA5 PRELIMINARY; PRT; 540 AA.
AC Q9AFA5;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Tsukamurellaceae; Tsukamurella.
NCBI_Taxid=2061;

RM
RN
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam; PF00118; cpn60_TCPL_1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 122; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 9, 1e-11;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAPTTNDG 22
DB 31 GPKGRNVLEKKWGAPTTNDG 52

RESULT 5
Q9KGW1 PRELIMINARY; PRT; 541 AA.
AC Q9KGW1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
NCBI_Taxid=1764;

RM
RN
RP SEQUENCE FROM N.A.
RA Nagabhushanam V., Praszkier J., Cheers C.;
RT "Molecular and immunological characterization of the M. avium homolog
RL of Hsp65.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 10.6667 seconds
(without alignments)
144.134 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: PIR-71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	540	2 A26950	groEL2 protein - M
2	90	100.0	540	2 A43509	65K antigen mbaa -
3	90	100.0	540	2 C41325	heat shock protein
4	90	100.0	541	2 S40245	heat shock protein
5	90	100.0	541	2 T44725	chaperonin 60K [im
6	90	100.0	588	2 A25902	65K antigen - Myco
7	81	90.0	543	2 S70013	chaperonin-like pr
8	80	88.9	528	2 S73270	chaperonin, 60K -
9	80	88.9	538	2 H72367	groEL protein - Th
10	80	88.9	541	2 T06829	chaperonin groEL -
11	80	88.9	541	1 BYYCGL	chaperonin groEL -
12	80	88.9	544	2 AG2263	chaperonin groEL -
13	79	87.8	577	2 S20876	chaperonin hsp60 p
14	78	86.7	524	2 F84742	mitochondrial chap
15	77	85.6	538	2 JQ1195	heat shock protein
16	77	85.6	539	2 B49855	heat shock protein
17	77	85.6	541	2 B44425	chaperonin groEL -
18	77	85.6	542	2 AC1704	class I heat-shock
19	77	85.6	542	2 AD1333	class I heat-shock
20	77	85.6	543	2 B41872	heat shock protein
21	77	85.6	543	2 F97232	chaperonin groEL,
22	77	85.6	544	2 JC5130	heat shock protein
23	77	85.6	544	2 B41884	58K heat shock pro
24	77	85.6	544	2 JC6063	chaperonin groEL -
25	77	85.6	544	2 B83720	class I heat-shock
26	76	84.4	599	2 T07753	probable chaperon
27	75	83.3	540	2 B41325	heat shock protein
28	75	83.3	541	2 T35591	chaperonin cpn60 -
29	75	83.3	546	2 S34938	heat shock protein

30	75	83.3	546	2 B47073	chaperonin groEL -
31	74	82.2	534	2 S26877	groEL protein - re
32	74	82.2	541	2 S68249	chaperonin groEL h
33	74	82.2	552	2 S74322	chaperonin groEL-2
34	74	82.2	560	2 AB2043	chaperonin groEL 1
35	73	81.1	174	2 T07736	probable chaperon1
36	73	81.1	539	2 S22342	chaperonin hsp60 -
37	73	81.1	542	2 JN0661	heat shock protein
38	73	81.1	542	2 S32106	groEL protein - la
39	73	81.1	546	2 B86674	60 kD chaperonin 1
40	73	81.1	542	2 I40342	heat shock protein
41	73	81.1	546	2 S22347	groEL - Brucella a
42	73	81.1	546	2 AG3640	60K chaperonin gro
43	73	81.1	547	2 B87334	chaperonin, 60 kDa
44	73	81.1	550	2 A41468	60K heat shock pro
45	73	81.1	588	2 PW0007	chaperonin 62.5K b

ALIGNMENTS

RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
N:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J. Bacteriol. 169, 1080-1088, 1987
A>Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; MUID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SH>
A:Cross-references: GB:M15467; NID:9149999; PIDN:AAA8232.1; PID:9150000
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
: Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Kajandrem, W.A.; Rogers, R.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A>Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295587
A:Accession: A70830
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-540 <CO>
A:Cross-references: GB:AL021932; GB:AL123456; NID:93261527; PIDN:CAI7397.1; PID:9290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; Rv0440
C:Superfamily: chaperonin groEL
Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKMGAP 16
DB 31 GPKGRNVLEKKMGAP 46
RESULT 2
A43509
65K antigen mbaa - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Thole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Berwald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A>Title: Characterization, sequence determination, and immunogenicity of a 64-kilodal
A:Reference number: A43509; MUID:87193155
A:Accession: A43509

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA25358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
|||||
DB 31 GPKGRNVLEKKWGAP 46

RESULT 3

heat shock protein 56 - Streptomyces albus
Alternate names: heat shock protein groEL homolog 2

C:Species: Streptomyces albus

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999

C:Accession: C41325

R:Maizdier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.

J. Bacteriol. 173, 7382-7386, 1991

A:Title: Characterization of the groEL-like genes in Streptomyces albus.

A:Reference number: A41325; MUID:92041639

A:Accession: C41325

A:Molecule type: DNA

A:Residues: 1-540 <MAZ>

A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294

C:Genetics:

A:Gene: groEL2

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
|||||
DB 31 GPKGRNVLEKKWGAP 46

RESULT 4

S40245

heat shock protein 65 - Mycobacterium paratuberculosis

C:Species: Mycobacterium paratuberculosis

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999

C:Accession: S40245

R:Colston, X.Y.Z.; McConnell, X.Y.Z.; Bujdoso, R.

submitted to the EMBL Data Library, August 1993

A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.

A:Reference number: S40245

A:Accession: S40245

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-541 <COL>

A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
|||||
DB 31 GPKGRNVLEKKWGAP 46

RESULT 5

T44725

chaperonin 60K [imported] - Mycobacterium leprae

Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44725
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998

A:Reference number: Z22831

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-541 <JAM>

A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1

A:Experimental source: cosmid B1450

C:Genetics:

A:Gene: groEL-2

C:Superfamily: chaperonin groEL

C:Keywords: molecular chaperone

Query Match 100.0%; Score 90; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 5.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
|||||
DB 31 GPKGRNVLEKKWGAP 46

RESULT 6

A25902

65K antigen - Mycobacterium leprae

C:Species: Mycobacterium leprae

C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997

C:Accession: A25902

R:Mehta, V.; Sweetser, D.; Young, R.A.

Proc. Natl. Acad. Sci. U.S.A. 83, 7013-7017, 1986

A:Title: Efficient mapping of protein antigenic determinants.

A:Reference number: A25902; MUID:86313701

A:Accession: A25902

A:Molecule type: DNA

A:Residues: 1-588 <MEH>

C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 90; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGAP 16
|||||
DB 78 GPKGRNVLEKKWGAP 93

RESULT 7

S70013

chaperonin-like protein groEL2 - Synechococcus sp.

C:Species: Synechococcus sp.

C:Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 20-Jun-2000

C:Accession: S70013; S70022

R:Furuki, M.; Tanaka, N.; Hiyaama, T.; Nakamoto, H.

Biochim. Biophys. Acta 1294, 106-110, 1996

A:Title: Cloning, characterization and functional analysis of groEL-like gene from th

A:Reference number: S70013; MUID:96248387

A:Accession: S70013

A:Molecule type: DNA

A:Residues: 1-543 <FUR>

A:Cross-references: GB:D86384; EMBL:DI7354; NID:g1408522; PIDN:BA113082.1; PID:g12280

A:Note: the source is designated as Synechococcus vulcanus

A:Accession: S70022

A:Molecule type: protein

A:Residues: 2-11 <FUR>

A:Note: the source is designated as Synechococcus vulcanus

C:Genetics:

A:Gene: groEL2

C:Superfamily: chaperonin groEL

C:Keywords: heat shock

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 5.62963 Seconds
(without alignments) 110.045 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVYLEKKGAP 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	ID	Description
1	90	100.0	476	CH62_STRLI	O33658 streptomyc
2	90	100.0	539	CH62_MYCBU	P06806 mycobacteri
3	90	100.0	539	CH62_STRLI	Q00768 streptomyc
4	90	100.0	540	CH60_MYCPA	P42384 mycobacteri
5	90	100.0	540	CH62_MYCLE	P09239 mycobacteri
6	81	90.0	543	CH62_STYNU	Q57002 streptococc
7	80	88.9	300	CH60_STYNU	P12834 streptococc
8	80	88.9	528	CH60_PORPU	P51349 porphyra pu
9	80	88.9	538	CH60_THEMA	Q09yx6 thermotoga
10	80	88.9	541	CH60_CYAPA	Q37757 cyanophora
11	80	88.9	544	CH60_STYNU	P22879 streptococc
12	80	88.9	544	CH61_STYNU	O50323 streptococc
13	78	87.8	577	CH60_ARATH	P28197 arabidopsis
14	78	86.7	529	CH60_GUITH	Q78419 guillardia
15	77	85.6	538	CH60_BACP3	P28209 bacillus ps
16	77	85.6	539	CH60_BACP3	007201 bacillus st
17	77	85.6	540	CH61_STYNU	O05972 streptocyst
18	77	85.6	543	CH60_BACSU	P28598 bacillus su
19	77	85.6	543	CH60_CLOAB	P30717 clostridium
20	77	85.6	544	CH60_BACD	O50303 bacillus ha
21	76	84.4	530	CH60_CYACA	O95121 cyanidium c
22	75	83.3	539	CH61_STRLI	Q00767 streptomyc
23	75	83.3	540	CH61_STRGO	P40171 streptomyc
24	75	83.3	546	CH60_CHRYI	P31293 chrometium
25	75	83.3	546	CH60_LEPST	P35468 leptospira
26	75	83.3	552	CH60_PSEST	O33500 pseudomonas
27	75	83.3	568	CH60_CAEEL	P50140 caenorhabdi
28	75	83.3	573	CH60_DROME	O02649 drosophila
29	75	83.3	573	CH6C_DROME	O9ymms drosophila
30	74	82.2	534	CH60_GALSU	P28256 galidieria s
31	74	82.2	540	CH60_CLOTH	P48212 clostridium
32	74	82.2	542	CH60_THERH	P45746 thermus aqu
33	74	82.2	551	CH62_STYNU	P22034 streptocyst

34	73	81.1	539	1	CH60_CLOPE	P26821 clostridium
35	73	81.1	539	1	CH61_BRAVA	P77829 bradyrhizob
36	73	81.1	542	1	CH60_LACIA	P37282 lactococcus
37	73	81.1	545	1	CH60_RHOCA	P95678 rhodobacter
38	73	81.1	546	1	CH60_BRUAB	P25967 brucella ab
39	73	81.1	547	1	CH60_CAUCR	P48211 caulobacter
40	73	81.1	547	1	CH60_LEGNA	P26878 legionella
41	73	81.1	588	1	RUBB_BRANA	P21241 brassica na
42	73	81.1	595	1	RUBB_PEA	P08927 pisum sativ
43	73	81.1	608	1	RUBB_ARATH	P21240 arabidopsis
44	72	80.0	520	1	CH60_ODOSI	P49464 odontella s
45	72	80.0	539	1	CH60_ENTAG	O66200 enterobacte

ALIGNMENTS

RESULT 1

CH62_STRLI STANDARD: PRT: 476 AA.

AC O33658: 16-OCT-2001 (rel. 40, Created)

DT 16-OCT-2001 (rel. 40, Last sequence update)

DT 16-OCT-2001 (rel. 40, Last annotation update)

DE 60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).

GN GROEL2 OR GROEL2.

OS Streptomyces lividans.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1916;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TK21;

RX MEDLINE=98048481; PubMed=9387235;

RA de Leon P., Marco S., Isiegas C., Marina A., Carrascosa J.L.,

RA Mellado R.P.;

RT "Streptomyces lividans groes, groEL1 and groEL2 genes.";

RL Microbiology 143:3563-3571(1997).

CC -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS

CC CONDITIONS (BY SIMILARITY).

CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF

CC 7 SUBUNITS (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.

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CC -----

CC EMBL: X95971; CAA65226.1; -

DR HSSP: P45746; ISRV.

DR InterPro: IPR001844; Chaperonins_cpn60.

DR InterPro: IPR002423; TCP1_cpn60.

DR Pfam: PF00118; cpn60_TCP1; 1.

DR PRINTS: PR00298; CHAPERONIN60.

DR PRINTS: PR00304; TCOMPLEXTCP1.

DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.

KW Chaperone; ATP-binding; Multigene family.

FT INT_MFE 0

FT SEQUENCE 476 AA: 50529 MW: 760F81793F4FED4D CRC64;

QY 1 GPKGRNVYLEKKGAP 16

DB 30 GPKGRNVYLEKKGAP 45

Query Match 100.0%; Score 90; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2

ID	CH62_MYCTU	STANDARD:	PRT:	539 AA.
AC	P06806;	Q48920;		
DT	01-Jan-1988	(Rel. 06, Created)		
DT	01-Oct-1996	(Rel. 34, Last sequence update)		
DT	16-Oct-2001	(Rel. 40, Last annotation update)		
DE	60 kDa chaparomn 2 (protein Cpn60-2) (groEL protein 2) (65 kDa			
DE	aragen) (Heat shock protein 65) (cell wall protein A) (antigen A)			
GN	groL2 OR groEL2 OR groEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT0357.04.			
OS	Mycobacterium tuberculosis, and			
OS	Mycobacterium bovis.			
OC	Bacteria; Firmicutes; Corynebacterineae; Mycobacteriaceae;			
OC	Actinomycetales; Corynebacteriaceae; Mycobacterium.			
OX	NCBI_TaxID=1773. 1765;			
RN	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=ERDMANN;			
RC	MEDLINE=87137260; Pubmed=3029018;			
RT	Shimnick T.M.;			
RT	"The 65-kilodalton antigen of Mycobacterium tuberculosis.";			
RL	J. Bacteriol. 169:1080-1088(1987).			
RN	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=H37RV;			
RC	MEDLINE=98295987; Pubmed=9634230;			
RA	Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,			
RA	Gordon S.V., Elismeyer K., Gas S., Barry C.E. III, Tekala F.,			
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,			
RA	Davies R., Devlin K., Feltham T., Gentles S., Hamlin N., Holroyd S.,			
RA	Hornsby T., Jagski K., Krogh A., McLean J., Moulie S., Murphy L.,			
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,			
RA	Rutter S., Seeger K., Skellern S., Squares S., Squares R.,			
RA	Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;			
RT	"Deciphering the biology of Mycobacterium tuberculosis from the			
RT	complete genome sequence.";			
RL	Nature 393:537-544(1998).			
RN	SEQUENCE FROM N.A.			
RC	SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;			
RC	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,			
RA	Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,			
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,			
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,			
RA	Bissh W.;			
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and			
RT	laboratory strains.";			
RL	Submitted (APR-2001) to the EMBL/Genbank/DBJ databases.			
RN	SEQUENCE FROM N.A.			
RC	SPECIES=M.bovis; STRAIN=BCG;			
RC	MEDLINE=87193155; Pubmed=3553003;			
RA	Thole J.E.R., Keulen W.J., Kolk A.H.J., Grootuis D.G., Berauld L.G.,			
RA	Tiesjema R.H., van Embden J.D.A.;			
RT	"Characterization, sequence determination, and immunogenicity of a			
RT	64-kilodalton protein of Mycobacterium bovis BCG expressed in			
RT	Escherichia coli K-12.";			
RL	Infect. Immun. 55:1466-1475(1987).			
RN	SEQUENCE OF 45-195 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;			
RC	Ros C., Belak K.;			
RL	Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.			
RN	SEQUENCE OF 63-182 FROM N.A.			
RC	SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMC1024;			
RC	MEDLINE=95150784; Pubmed=7848059;			
RA	Kapur V., Li L.L., Hamrick M.R., Pitkaytis B.B., Shimnick T.M.,			
RA	Telenti A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y.,			
RA	Claridge J.E., Kreiswirth B.N., Musser J.M.;			
RT	"Rapid Mycobacterium species associated with antimicrobial resistance			
RT	Identification of mutations associated with antimicrobial resistance			

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RT      In Mycobacterium tuberculosis by automated DNA sequencing.";
RN      Arch. Pathol. Lab. Med. 119:131-138(1995).
RP      SEQUENCE OF 64-177 FROM N.A.
RC      SPECIES=M.tuberculosis;
RX      MEDLINE=95214306; PubMed=7699930;
RA      Hataka E., Ueno I., Kawakami Y., Furuwatari C., Furihata K.,
RT      Katsuyama T.;
RT      "Detection and identification of mycobacteria by PCR-RFLP method.";
RL      Risho Biyori 43:155-161(1995)
CC      FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOOLDING AND
CC      PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC      CONDITIONS (BY SIMILARITY).
CC      -1 SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC      7 SUBUNITS (BY SIMILARITY).
CC      -1 MISCELLANEOUS: PURIFIED 65 kDa ANTIGEN CAN ELICIT A STRONG
CC      DELAYED-TYPE HYPERSENSITIVITY REACTION IN EXPERIMENTAL ANIMALS
CC      INFECTED WITH M.TUBERCULOSIS. THIS PROTEIN IS ONE OF THE MAJOR
CC      IMMUNOREACTIVE PROTEINS OF THE MYCOBACTERIA. THIS ANTIGEN CONTAINS
CC      EPITOPEs THAT ARE COMMON TO VARIOUS SPECIES OF MYCOBACTERIA.
CC      -1 SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC      -----
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CC      -----
DR      EMBL, M15467; AAA88232.1; -.
DR      EMBL, AL021932; CAAL17397.1; -.
DR      EMBL, AE006948; AAK44679.1; -.
DR      EMBL, M17705; AAA25358.1; -.
DR      EMBL, U55833; AAC44451.1; -.
DR      EMBL, U55825; AAC44458.1; -.
DR      EMBL, U17925; AAB39044.1; -.
DR      EMBL, U17957; AAB39076.1; -.
DR      EMBL, S76635; -, NOT_ANNOTATED_CDS.
DR      PIR, A26950; A26950.
DR      PIR, A43509; A43509.
DR      HSSP: P45746; ISRV.
DR      TIGR: MT0456; -.
DR      Tubercultist; RV0440; -.
DR      InterPro: IPR001844; Chaperonins_cpn60.
DR      InterPro: IPR002423; TCPL_cpn60.
DR      Pfam: PF00118; cpn60_TCPL_1.
DR      PRINTS: PR00298; CHAPERONIN60.
DR      PRINTS: PR00304; TCOMPLEXTCPL.
DR      PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW      Chaperone; ATP-binding; Multigene family; Antigen; Cell wall;
KW      Complete proteome.
FT      INIT_MOTIF 0
SQ      SEQUENCE 539 AA; 56595 MW; PF03460BAAZDC557 CRC64;
OY      1 GPKGRNVYLEKKWAP 16
DB      30 GPKGRNVYLEKKWAP 45
ID      CH62_STRAL STANDARD; PRT; 539 AA.
AC      Q00768;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL protein 2) (HSP56).
GN      GROEL2 OR GROEL2.

```

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 18.0741 Seconds
(without alignments) 153.143 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

1 number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	90	100.0	59	2	Q9EMD1	Q9ewd1 streptomyc
2	90	100.0	61	2	Q9EUR7	Q9eur7 streptomyc
3	90	100.0	539	2	P97086	P97086 tsukamurell
4	90	100.0	540	2	Q9AFAS	Q9afas tsukamurell
5	90	100.0	541	2	Q9KGM1	Q9kgm1 mycobacteri
6	90	100.0	541	2	Q9AFAS	Q9afas nocardia fa
7	90	100.0	541	2	Q9KXU5	Q9kxu5 streptomyc
8	90	100.0	541	2	Q9KQ12	Q9kq12 corynebacte
9	90	100.0	542	2	Q9AFCS	Q9afcs nocardia as
10	85	94.4	533	2	Q9FDS2	Q9fds2 propionibac
11	85	94.4	544	2	Q9K2U4	Q9k2u4 propionibac
12	81	90.0	543	2	Q9AMJ8	Q9amj8 anaeroba sp
13	80	88.9	538	2	Q9EZV1	Q9ezv1 thermotoga
14	79	87.8	544	2	Q9XYR3	Q9xyr3 bacteroides
15	78	86.7	524	10	Q9KX14	Q9kx14 arabidopsis
16	77	85.6	539	2	Q9RC20	Q9rc20 bacillus sp

17	77	85.6	539	2	Q9EZY4	Q9EZY4 bacillus st
18	77	85.6	540	2	Q9XCA9	Q9XCA9 rhodothermu
19	77	85.6	542	2	Q9AGB6	Q9AGB6 listeria mo
20	77	85.6	542	16	Q929V0	Q929V0 listeria in
21	77	85.6	581	5	Q46219	Q46219 culicoides
22	76	84.4	543	2	Q9KJ23	Q9KJ23 lactobacill
23	76	84.4	598	5	Q9XVR7	Q9XVR7 onchocerca
24	76	84.4	599	10	P93570	P93570 solanum tub
25	75	83.3	546	2	Q11198	Q11198 leptospira
26	75	83.3	568	5	Q96500	Q96500 caenorhabdi
27	75	83.3	573	5	Q9U5N2	Q9U5N2 myzus persi
28	75	83.3	580	5	Q96783	Q96783 plectus acu
29	75	83.3	582	5	Q9U5L7	Q9U5L7 paracentrot
30	73	81.1	174	10	P93571	P93571 solanum tub
31	73	81.1	537	2	Q9K171	Q9K171 bifidobacte
32	73	81.1	540	2	Q9K170	Q9K170 bifidobacte
33	73	81.1	541	2	Q9K177	Q9K177 clostridium
34	73	81.1	541	2	Q9K157	Q9K157 gardnerella
35	73	81.1	542	2	Q9AEP7	Q9AEP7 lactococcus
36	73	81.1	555	2	Q9X603	Q9X603 primary end
37	73	81.1	596	10	Q9FHA9	Q9FHA9 arabidopsis
38	73	81.1	596	10	Q9LJE4	Q9LJE4 arabidopsis
39	73	81.1	600	10	Q9SAV2	Q9SAV2 arabidopsis
40	73	81.1	601	10	Q9LWT6	Q9LWT6 oryza sativ
41	72	80.0	82	2	Q9F4F1	Q9F4F1 buchnera ap
42	72	80.0	82	2	Q9F4E9	Q9F4E9 buchnera ap
43	72	80.0	82	2	Q9F4E7	Q9F4E7 buchnera ap
44	72	80.0	82	2	Q9F4E5	Q9F4E5 buchnera ap
45	72	80.0	82	2	Q9F4E3	Q9F4E3 buchnera ap

ALIGNMENTS

RESULT 1
ID Q9EMD1 PRELIMINARY: PRT: 59 AA.
AC Q9EMD1.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycetales; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=J802.
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.,
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis.";
RL Submitted (Oct-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ250536; CAC19351.1; -
DR HSP: P06139; IAO:
DR InterPro: IPR002423; TCPL-CPN60.
DR Pfam: PF00118; CPN60_TCP1; 1.
DR PRINTS: PR00304; TCOMPLEXTCP1.
KW ATP-binding; Chaperone.
FT NON-TER 59
SQ SEQUENCE 59 AA: 6407 MW: E7B24199B7DE68FA CRC64;
Query Match 100.0%; Score 90; DB 2; Length 59;
Best Local Similarity 100.0%; Pred. No. 5e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKMGAP 16
DB 31 GPKGRNVLEKKMGAP 46
RESULT 2

09EUR7
ID 09EUR7 PRELIMINARY; PRT; 61 AA.
AC 09EUR7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
antibiotic biosynthesis.";
RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RI EMBL; AJ250537; CAC19355.1; -.
RS HSP; P06139; IAOB.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL.1.
DR PRINTS; PR00304; TCOMPLEXTCPL.
KW ATP-binding; Chaperone.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6645 MW; D200955F4199B7CA CRC64;
Query Match 100.0%; Score 90; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 5.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16
DB 31 GPKGRNVLEKKWGAP 46
RESULT 3
P97086 PRELIMINARY; PRT; 539 AA.
AC P97086;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMIB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
protein 60.";
RT Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; U90204; AAB49990.1; -.
DR HSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
FT SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

Query Match 100.0%; Score 90; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16
DB 31 GPKGRNVLEKKWGAP 46
RESULT 4
Q9AFAS PRELIMINARY; PRT; 540 AA.
AC Q9AFAS;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene.";
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -1- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR EMBL; AF352578; AAK18614.1; -.
DR HSP; P06139; IGRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPL.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
FT SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;
Query Match 100.0%; Score 90; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 5.6e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16
DB 31 GPKGRNVLEKKWGAP 46
RESULT 5
Q9KGW1 PRELIMINARY; PRT; 541 AA.
AC Q9KGW1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagabushanam V., Praszkier J., Cheers C.;
RT "Molecular and immunological characterization of the M. avium homolog
of Hsp65.";
RT Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 : Search time 22.5185 Seconds
(without alignments)
78.921 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues 747574

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A.GeneSeq_032802:*

1: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*

3: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

4: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

5: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*

6: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1987.DAT:*

9: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1988.DAT:*

10: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1989.DAT:*

11: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1990.DAT:*

12: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1991.DAT:*

13: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*

14: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1993.DAT:*

15: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1994.DAT:*

16: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1995.DAT:*

17: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*

18: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*

19: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*

20: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	21	AAV93329
2	90	100.0	22	21	AAV93328
3	90	100.0	215	19	AAW60145
4	90	100.0	215	20	AAV14892
5	90	100.0	295	22	AAAB31615
6	90	100.0	523	19	AAW60144
7	90	100.0	523	20	AAV14891
8	90	100.0	539	20	AAV23919
9	90	100.0	540	9	AAAB1351
10	90	100.0	540	16	AAW81610
11	90	100.0	540	18	AAW32100

12	90	100.0	540	19	AAW44702	Mycobacterium tube
13	90	100.0	540	20	AAV23911	Amino acid sequenc
14	90	100.0	540	21	AAV93332	Amino acid sequenc
15	90	100.0	540	22	AAE11755	Mycobacterium tube
16	90	100.0	540	22	AAW81118	Mycobacterium tube
17	90	100.0	540	22	AAAB31606	Amino acid sequenc
18	90	100.0	541	16	AAW67384	M. leprae GroEL 1 g
19	90	100.0	541	20	AAV14909	Amino acid sequenc
20	90	100.0	541	20	AAV23910	Amino acid sequenc
21	90	100.0	541	20	AAV23913	Amino acid sequenc
22	90	100.0	544	18	AAW32099	Mycobacteria sp. h
23	90	100.0	560	9	AAW80215	Sequence of Mycoba
24	90	100.0	572	11	AAW04716	Amino acid sequenc
25	90	100.0	573	11	AAW04715	Amino acid sequenc
26	90	100.0	573	16	AAW64765	M. leprae 65 kDa p
27	90	100.0	573	16	AAW64766	M. tuberculosis 65
28	90	100.0	588	9	AAW80364	M. leprae 65KD ant
29	90	100.0	638	21	AAW03790	Heat shock protein
30	90	100.0	639	22	AAW31609	Amino acid sequenc
31	90	100.0	648	22	AAW31614	Amino acid sequenc
32	90	100.0	948	22	AAW31611	Amino acid sequenc
33	85	94.4	612	22	AAW63908	Propionibacterium
34	84	93.3	548	17	AAW94368	Brevibacterium fla
35	84	93.3	548	22	AAW92732	C glutamylum prote
36	83	92.2	15	17	AAW94779	Peptide from libra
37	83	92.2	15	18	AAW43457	Mycobacteria sp. h
38	79	87.8	95	22	AAW56597	Propionibacterium
39	79	87.8	577	20	AAV23927	Amino acid sequenc
40	77	85.6	52	13	AAW20195	Heat shock protein
41	77	85.6	541	20	AAV23917	Amino acid sequenc
42	77	85.6	544	20	AAV23905	Amino acid sequenc
43	75	83.3	440	13	AAW22362	GroEL-1 protein pa
44	75	83.3	540	13	AAW22363	GroEL-1 protein
45	75	83.3	545	20	AAV23930	Consensus mmo aci

ALIGNMENTS

RESULT 1

AAV93329 standard; peptide; 16 AA.

AAV93329;

04-SEP-2000 (first entry)

Amino acid sequence of an epitope of heat shock protein 60.

Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;

Inflammatory disorder; arthritis.

Mycobacterium tuberculosis.

WO200027870-A1.

18-MAY-2000.

04-NOV-1999; 99WO-IL00595.

05-NOV-1998; 98US-0107213.

(HADA-) HADASIT MEDICAL RES SERVICES & DEV.

Naparstek Y, Ulmansky R, Kashi Y;

WPI; 2000-376486/32.

Peptide having a defined sequence is used in vaccines for conferring

immunity against autoimmune disease or inflammatory disorders,

especially arthritis.

Claim 2; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX

SO Sequence 16 AA;

Query Match 100.0%; Score 90; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8e-09;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16
 |||||
 DB 1 GPKGRNVLEKKMGAP 16

LT 2
 3328
 ID AAY93328 standard: peptide; 22 AA.
 AC AAY93328;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

XX Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 KM inflammatory disorder; arthritis.

OS Mycobacterium tuberculosis.

PN WO200027870-A1.

XX 18-MAY-2000.

PF 04-NOV-1999; 99WO-IL00595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

PI Naparstek Y, Ulmansky R, Kashi Y;

DR WPI; 2000-376486/32.

XX Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -

PS Claim 1; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 XX

SO Sequence 22 AA;

Query Match 100.0%; Score 90; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 1.1e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16
 |||||
 DB 1 GPKGRNVLEKKMGAP 16

RESULT 3

AAW60145
 ID AAW60145 standard: Protein; 215 AA.
 XX

AC AAW60145;

DT 25-AUG-1998 (first entry)

DE M. vaccae antigen GV-27A sequence.

XX Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
 KM mycobacteria infection; vaccine; cancer.

OS Mycobacterium vaccae.

PN WO9808542-A2.

PD 05-MAR-1998.

PF 28-AUG-1997; 97WO-N200105.

PR 12-JUN-1997; 97US-0873970.

PR 29-AUG-1996; 96US-0705347.

PA (GENE-) GENESIS RES & DEV CORP.

PI Hiyama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

DR Visser E;

DR WPI; 1998-216926/19.

DR N-PSDB; AAV34609.

XX Mycobacterium vaccae polypeptides - used to develop products for use

PT in detection, therapy and prevention of mycobacteria infections or

PT as immune response enhancers

PS Claim 48; Pages 117-118; 153pp; English.

XX This represents a Mycobacterium vaccae antigen GV-27A. The invention
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an
 CC immune response in patients previously exposed to a mycobacterium. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
 CC B cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.
 XX

SO Sequence 215 AA;

Query Match 100.0%; Score 90; DB 19; Length 215;
 Best Local Similarity 100.0%; Pred. No. 1.4e-07;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKMGAP 16
 |||||
 DB 31 GPKGRNVLEKKMGAP 46

RESULT 4

AAV14892
 ID AAV14892 standard: protein; 215 AA.

AC AAV14892;

DT 25-OCT-1999 (first entry)

DE Amino acid sequence of M. vaccae antigen GV-27A.

XX Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 9.48148 Seconds
(without alignments)
41.218 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKWGAP 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

1 number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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- 2: /cgn2_6/p/tdata/1/1aa/5B.COMB.pep.*
- 3: /cgn2_6/p/tdata/1/1aa/6A.COMB.pep.*
- 4: /cgn2_6/p/tdata/1/1aa/6B.COMB.pep.*
- 5: /cgn2_6/p/tdata/1/1aa/PCTUS.COMB.pep.*
- 6: /cgn2_6/p/tdata/1/1aa/backfill1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	90	100.0	215	2	US-08-997-080-117
2	90	100.0	215	2	US-08-997-362-117
3	90	100.0	215	4	US-09-095-855-117
4	90	100.0	215	4	US-09-324-542-117
5	90	100.0	215	2	US-08-997-080-114
6	90	100.0	523	2	US-08-997-362-114
7	90	100.0	523	4	US-09-095-855-114
8	90	100.0	523	4	US-09-324-542-114
9	90	100.0	540	2	US-08-368-834-20
10	90	100.0	540	4	US-08-461-722-3
11	90	100.0	540	4	US-08-461-722-4
12	90	100.0	540	4	US-08-336-251-3
13	90	100.0	540	4	US-08-336-251-4
14	90	100.0	540	5	PCT-US94-06362-3
15	90	100.0	540	5	PCT-US94-06362-4
16	90	100.0	541	2	US-08-467-822-34
17	90	100.0	541	2	US-08-447-154-19
18	90	100.0	541	2	US-08-997-080-160
19	90	100.0	541	2	US-08-997-362-160
20	90	100.0	541	2	US-09-095-855-160
21	90	100.0	541	4	US-08-432-697-34
22	90	100.0	541	4	US-08-466-248-34
23	90	100.0	541	4	US-09-324-542-160
24	73	81.1	548	2	US-08-467-822-31
25	73	81.1	548	4	US-08-432-697-31
26	73	81.1	548	4	US-08-466-248-31
27	72	80.0	547	4	US-08-461-722-2

28	72	80.0	547	4	US-08-336-251-2	Sequence 2, Appl1
29	72	80.0	547	5	PCT-US94-06362-2	Sequence 2, Appl1
30	72	80.0	548	2	US-08-467-822-32	Sequence 32, Appl1
31	72	80.0	548	4	US-09-472-971-3	Sequence 3, Appl1
32	72	80.0	548	4	US-08-432-697-32	Sequence 32, Appl1
33	72	80.0	548	4	US-08-466-248-32	Sequence 32, Appl1
34	69	76.7	547	2	US-08-467-822-35	Sequence 35, Appl1
35	69	76.7	547	4	US-08-432-697-35	Sequence 35, Appl1
36	69	76.7	547	4	US-08-466-248-35	Sequence 35, Appl1
37	69	76.7	573	4	US-08-461-722-1	Sequence 1, Appl1
38	69	76.7	573	4	US-08-336-251-1	Sequence 1, Appl1
39	69	76.7	573	5	PCT-US94-06362-1	Sequence 1, Appl1
40	67	74.4	573	2	US-08-706-209-1	Sequence 1, Appl1
41	67	74.4	573	3	US-08-981-787-1	Sequence 1, Appl1
42	67	74.4	573	5	PCT-US96-11373-1	Sequence 1, Appl1
43	67	74.4	573	5	PCT-US96-11375-1	Sequence 1, Appl1
44	65	72.2	545	2	US-08-467-822-30	Sequence 30, Appl1
45	65	72.2	545	4	US-08-432-697-30	Sequence 30, Appl1

ALIGNMENTS

RESULT 1
US-08-997-080-117
Sequence 117, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-117
Query Match 100.0%; Score 90; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPKGRNVLEKKWGAP 16

Db 31 GPKGRNVLEKKWGP 46

RESULT 2

US-08-997-362-117
Sequence 117, Application US/08997362
Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul
APPLICANT: Hiya, Jun
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot
APPLICANT: Scott, Linda
APPLICANT: Prestidge, Ross
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
FILING DATE: June 12, 1997
APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000,1002c2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-362-117

Query Match 100.0%; Score 90; DB 2; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGP 16
Db 31 GPKGRNVLEKKWGP 46

RESULT 3

US-09-095-855-117
Sequence 117, Application US/09095855
Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul
APPLICANT: Visser, Elizabeth
APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross
TITLE OF INVENTION: Compounds and Methods for
Treatment and Diagnosis of Mycobacterial Infections
NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/095,855
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347
FILING DATE: 29-AUG-1996
APPLICATION NUMBER: 08/873,970
FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362
FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000,1002c3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-095-855-117

Query Match 100.0%; Score 90; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 4.3e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPKGRNVLEKKWGP 16
Db 31 GPKGRNVLEKKWGP 46

RESULT 4

US-09-324-542-117
Sequence 117, Application US/09324542
Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Tan, Paul L.J.
APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment
of Immunologically-Mediated Skin Disorders
FILE REFERENCE: 11000,1007c1

CURRENT APPLICATION NUMBER: US/09/324,542
CURRENT FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080
EARLIER FILING DATE: 1997-12-23

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 117
LENGTH: 215
TYPE: PRT

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:28:37 : Search time 30 Seconds
(without alignments)
81.454 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122
Sequence: 1 GPKGRNVLEKKWKCAPITINDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

al number of hits satisfying chosen parameters: 239801

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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6: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

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17: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	122	100.0	22	21	AAV93328	Amino acid sequence
2	90	73.8	16	21	AAV93329	Amino acid sequence
3	87	71.3	16	18	AAW43458	Mycobacterium sp. h
4	87	71.3	16	21	AAV93330	Amino acid sequence
5	83	68.0	15	17	AAV94779	Peptide from libra
6	83	68.0	15	18	AAW43457	Mycobacterium sp. h
7	82	67.2	16	17	AAV94780	Peptide from libra
8	70	57.4	15	18	AAW43459	Mycobacterium sp. h
9	65	53.3	15	17	AAV94781	Peptide from libra
10	59	48.4	20	21	AAV93331	Amino acid sequence
11	57	46.7	16	17	AAV94778	Peptide from libra

12	57	46.7	16	18	AAW43456	Mycobacterium sp. h
13	47	38.5	11	22	AAV88272	Hsp-65 peptide epi
14	43	35.2	10	22	AAV88269	Hsp-65 peptide epi
15	42	34.4	20	10	AAV91037	Amino acids 1021-1
16	42	34.4	20	19	AAV68089	Tetanus toxin T-ce
17	39	32.0	9	22	AAV88279	Hsp-65 peptide epi
18	39	32.0	16	18	AAW43460	Mycobacterium sp. h
19	39	32.0	17	17	AAV94777	Peptide from libra
20	39	32.0	17	18	AAW43455	Mycobacterium sp. h
21	36	29.5	20	22	AAV93610	Peptide #7116 enco
22	36	29.5	20	22	AAV60314	Human brain expres
23	36	29.5	20	22	AAV72948	Human bone marrow
24	36	29.5	20	22	AAW33173	Peptide #7210 enco
25	35	28.7	16	16	AAV87908	Bovine lactoferrin
26	35	28.7	16	17	AAV10516	Lactoferrin derive
27	35	28.7	18	15	AAV69354	Bovine lactoferrin
28	35	28.7	18	17	AAV10515	Lactoferrin derive
29	35	28.7	20	13	AAV21808	Anti microbial pep
30	35	28.7	20	14	AAV21809	Anti microbial pep
31	35	28.7	20	14	AAV44840	Lactoferrin-relate
32	35	28.7	20	15	AAV48528	Lactoferrin derive
33	35	28.7	20	15	AAV48529	Lactoferrin derive
34	35	28.7	20	15	AAV57459	Lactoferrin derive
35	35	28.7	20	15	AAV57460	Lactoferrin derive
36	35	28.7	20	16	AAV84696	Bovine lactoferrin
37	35	28.7	20	16	AAV84697	Bovine lactoferrin
38	35	28.7	20	16	AAV80261	Anti-parasitic lac
39	35	28.7	20	16	AAV80262	Anti-parasitic lac
40	35	28.7	20	17	AAV98552	Peptide for anti-u
41	35	28.7	20	17	AAV91851	Lactoferrin-derive
42	35	28.7	20	17	AAV03044	Lactoferrin-derive
43	35	28.7	20	17	AAV90606	Lactoferrin-derive
44	35	28.7	20	17	AAV87619	Lactoferrin-derive
45	35	28.7	20	17	AAV87620	Lactoferrin-derive

ALIGNMENTS

RESULT 1
AAV93328 standard; peptide; 22 AA.
XX
AC AAV93328:
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
XX
KM Inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200027870-A1.
XX
PD 18-MAY-2000.
XX
XX 04-NOV-1999; 99W0-IL00595.
XX
XX 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
XX
PI Naparstek Y, Ulmansky R, Kashi Y;
DR WPI; 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT immunity against autoimmune disease or inflammatory disorders,
PT especially arthritis -
XX
PS Claim 1: Page 7: 58pp: English.

XX The present sequence represents an epitope of the heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
CC nucleic acid encoding it, are useful in vaccines for conferring
CC immunity against autoimmune disease or inflammatory disorders,
CC especially arthritis. The peptide may also be used to raise
CC antibodies, which are then used for passive immunisation.
XX
SQ Sequence 22 AA;
Query Match 100.0%; Score 122; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.7e-13;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAPITNDG 22
DB 1 GPKGRNVLEKKWGAPITNDG 22
|||||
RESULT 2
AAV93329 standard; peptide; 16 AA.
XX AAY93329;
AC AAY93329;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW Inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200027870-A1.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-IL00595.
XX
PR 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
PI Naparstek Y, Ulmansky R, Kashi Y;
XX
DR WPI: 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT immunity against autoimmune disease or inflammatory disorders,
PT especially arthritis -
XX
PS Claim 2; Page 7; 58pp; English.
XX
CC The present sequence represents an epitope of the heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
CC nucleic acid encoding it, are useful in vaccines for conferring
CC immunity against autoimmune disease or inflammatory disorders,
CC especially arthritis. The peptide may also be used to raise
CC antibodies, which are then used for passive immunisation.
XX
SQ Sequence 16 AA;
Query Match 73.8%; Score 90; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVLEKKWGAP 16
DB 1 GPKGRNVLEKKWGAP 16
|||||
RESULT 3

AAW43458
ID AAW43458 standard; peptide; 16 AA.
XX
AC AAW43458;
XX
DT 08-APR-1998 (first entry)
XX
DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).
XX
KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
KW pristanic induced arthritis; PLA.
XX
OS Synthetic.
OS Mycobacteria sp.
XX
PN WO9711966-A1.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-GB02382.
XX
PR 27-SEP-1995; 95GB-0019737.
XX
PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
PI Elson CJ, Thompson JS;
XX
DR WPI: 1997-212851/19.
XX
PT Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
XX
PS Disclosure: Fig 1a; 91pp; English.
XX
CC This peptide is one of a library (see AAW43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristanic induced arthritis (PIA) in vitro,
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAW14948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
SQ Sequence 16 AA;
Query Match 71.3%; Score 87; DB 18; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 NVYLEKKWGAPITND 21
DB 1 NVYLEKKWGAPITND 16
|||||
RESULT 4
AAV93330 standard; peptide; 16 AA.
ID AAV93330
XX
AC AAV93330;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW inflammatory disorder; arthritis.
XX

```

OS   Mycobacterium tuberculosis.
XX
XX   WO200027870-A1.
XX
XX   18-MAY-2000.
XX
XX   04-NOV-1999: 99WO-IL000595.
XX
XX   05-NOV-1998: 98US-0107213.
XX
XX   (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX   Naparstek Y, Ulanovsky R, Kasht Y;
XX
XX   WPI; 2000-376486/32.
XX
XX   Peptide having a defined sequence is used in vaccines for conferring
XX   immunity against autoimmune disease or inflammatory disorders,
XX   especially arthritis -
XX
XX   Claim 3; Page 7; 58pp; English.
XX
XX   The present sequence represents an epitope of the heat shock protein
XX   60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
XX   nucleic acid encoding it, are useful in vaccines for conferring
XX   immunity against autoimmune disease or inflammatory disorders,
XX   especially arthritis. The peptide may also be used to raise
XX   antibodies, which are then used for passive immunisation.
XX
XX   Sequence 16 AA:
XX
XX   Query Match 71.3%; Score 87; DB 21; Length 16;
XX   Best Local Similarity 100.0%; Pred. No. 1.2e-07;
XX   Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 7 VVLEKRWGAPTTNDG 22
DB 1 VVLEKRWGAPTTNDG 16
XX
XX
XX   RESULT 5
XX   AAR94779
XX   ID AAR94779 standard; peptide; 15 AA.
XX
XX   AAR94779;
XX
XX   11-NOV-1996 (first entry)
XX
XX   Peptide from library spanning whole of hsp65.
XX
XX   Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX   Rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX   prophylaxis.
XX
XX   Synthetic.
XX
XX   WO9610039-A1.
XX
XX   04-APR-1996.
XX
XX   27-SEP-1995: 95WO-GB02295.
XX
XX   27-SEP-1994: 94GB-0019553.
XX
XX   (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX   Elson CJ, Thompson SJ;
XX
XX   WPI; 1996-200888/20.
XX
XX   Polypeptide derived from bacterial heat shock protein 65 - for use
XX   in diagnosis, prophylaxis and treatment of autoimmune disease e.g.
XX   Rheumatoid arthritis.

```

```

XX
XX   Example 1; Figure 1; 88pp; English.
XX
XX
XX   AAR94773-R94878 are overlapping peptides of a library spanning the
XX   whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX   prepared from the library and used to immunise mice. After 10 days the
XX   mice received injections of pristane to induce arthritis and the
XX   animals examined for incidence of arthritis. A preferred anti-arthritis
XX   peptide was found to correspond to residues 21-31 of full length hsp65
XX   (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX   treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX   diseases such as Rheumatoid arthritis.
XX
XX   Sequence 15 AA:
XX
XX   Query Match 68.0%; Score 83; DB 17; Length 15;
XX   Best Local Similarity 100.0%; Pred. No. 5.3e-07;
XX   Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GPKGRNVLEKKWGA 15
DB 1 GPKGRNVLEKKWGA 15
XX
XX
XX   RESULT 6
XX   AAM43457
XX   ID AAM43457 standard; peptide; 15 AA.
XX
XX   AAM43457;
XX
XX   08-APR-1998 (first entry)
XX
XX   Mycobacterium sp. hsp68 derived peptide (group 1 #77).
XX
XX
XX   Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
XX   Rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX   pristane induced arthritis; PIA.
XX
XX   Synthetic.
XX
XX   Mycobacteria sp.
XX
XX   WO9711966-A1.
XX
XX   03-APR-1997.
XX
XX   26-SEP-1996: 96WO-GB02382.
XX
XX   27-SEP-1995: 95GB-0019737.
XX
XX   (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX   Elson CJ, Thompson JS;
XX
XX   WPI; 1997-212851/19.
XX
XX   Polypeptide(s) derived from microbial heat shock protein - useful
XX   for treatment of autoimmune disease esp. arthritis
XX
XX   Disclosure; Fig 1a; 91pp; English.
XX
XX   This peptide is one of a library (see AAM43451-W43556) which represents
XX   the mycobacterial heat shock protein, hsp65 and is designed to study
XX   a novel method for the treatment of autoimmune disease e.g. Rheumatoid
XX   arthritis. This fragment has been allocated as a group 1 peptide which
XX   is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
XX   hsp65 is known to be an immunodominant antigen in a number of infectious
XX   diseases and is linked to pristane induced arthritis (PIA) in vitro.
XX   However heat shock proteins and peptides derived from microbial sources
XX   may act as self antigens and thus have limited clinical use. The human
XX   hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX   (see AAM14948-W14950) may be useful in the development of vaccines for
XX   prophylaxis or treatment of an autoimmune disease such as Rheumatoid
XX   arthritis.

```

```

XX Sequence 15 AA:
SQ
Query Match 68.0%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.3e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
    |||||
Db 1 GPKGRNVLEKKWGA 15

RESULT 7
AAR94780
ID AAR94780 standard; peptide; 16 AA.
XX
AC AAR94780;
XX
DF 11-NOV-1996 (first entry)
XX
    Peptide from library spanning whole of hsp65.
XX
KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX
PN WO9610039-A1.
XX
PD 04-APR-1996.
XX
PF 27-SEP-1995; 95WO-GB02295.
XX
PR 27-SEP-1994; 94GB-0019553.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Elson CJ, Thompson SJ;
XX
DR WPI; 1996-200888/20.
XX
    Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
PS Example 1; Figure 1; 88pp; English.
XX
    AAR94773-894878 are overlapping peptides of a library spanning the
    whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
    prepared from the library and used to immunise mice, after 10 days the
    mice received injections of pristane to induce arthritis and the
    CC animals examined for incidence of arthritis. A preferred anti-arthritis
    CC peptide was found to correspond to residues 21-31 of full length hsp65
    CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
    CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
    CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 16 AA:
Query Match 67.2%; Score 82; DB 17; Length 16;
Best Local Similarity 93.8%; Pred. No. 8.4e-07;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 6 NVYLEKKWGAPTTND 21
    |||||
Db 1 NVYLEKKWGAPTTND 16

RESULT 8
AAM43459
ID AAM43459 standard; peptide; 15 AA.
XX

```

```

AC AAM43459;
XX
DT 08-APR-1998 (first entry)
XX
DE Mycobacterium sp. hsp68 derived peptide (group 1 #9).
XX
KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
KW pristane induced arthritis; PIA.
XX
OS Synthetic.
OS Mycobacteria sp.
XX
PN WO9711966-A1.
XX
PD 03-APR-1997.
XX
PF 26-SEP-1996; 96WO-GB02382.
XX
PR 27-SEP-1995; 95GB-0019737.
XX
PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
PI Elson CJ, Thompson JS;
XX
DR WPI; 1997-212851/19.
XX
    Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
XX
PS Disclosure; Fig 1a; 91pp; English.
XX
    This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM14948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
SQ Sequence 15 AA:
Query Match 57.4%; Score 70; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAPTTNDG 22
    |||||
Db 1 KKWGAPTTNDG 12

RESULT 9
AAR94781
ID AAR94781 standard; peptide; 15 AA.
XX
AC AAR94781;
XX
DT 11-NOV-1996 (first entry)
XX
    Peptide from library spanning whole of hsp65.
XX
KW Hsp; heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX

```


PN WO9610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95WO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI: 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
XX Sequence 15 AA;
XX
XX Query Match 53.3%; Score 65; DB 17; Length 15;
XX Best Local Similarity 91.7%; Pred. No. 0.00053;
XX Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
OY 11 KKWGAPTTNDG 22
XX
XX Db 1 KKWGAPTTNDG 12
XX
XX
XX RESULT 10
XX AAY93331
XX ID AAY93331 standard; peptide; 20 AA.
XX
XX AC AAY93331;
XX
XX 04-SEP-2000 (first entry)
XX
XX Amino acid sequence of an epitope of heat shock protein 60.
XX
XX Eptope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
XX inflammatory disorder; arthritis.
XX
XX Homo sapiens.
XX
XX WO200027870-A1.
XX
XX PD 18-MAY-2000.
XX
XX PF 04-NOV-1999; 99WO-IL00595.
XX
XX PR 05-NOV-1998; 98US-0107213.
XX
XX PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
XX PI Naparstek Y, Ulimansky R, Kashi Y;
XX
XX WPI: 2000-376486/32.
XX
XX Peptide having a defined sequence is used in vaccines for conferring
XX immunity against autoimmune disease or inflammatory disorders,
XX especially arthritis -

XX
XX Claim 4; Page 7; 58pp; English.
XX
XX PS
XX CC The present sequence represents an epitope of the heat shock
XX protein 60 (Hsp60) of human origin. The peptide, and the
XX CC nucleic acid encoding it, are useful in vaccines for conferring
XX CC immunity against autoimmune disease or inflammatory disorders,
XX CC especially arthritis. The peptide may also be used to raise
XX CC antibodies, which are then used for passive immunisation.
XX
XX Sequence 20 AA;
XX
XX
XX Query Match 48.4%; Score 59; DB 21; Length 20;
XX Best Local Similarity 50.0%; Pred. No. 0.0074;
XX Matches 8; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
XX
OY 7 VLEKKWGAFTTNDG 22
XX
XX Db 2 VIEQSMGSPKVTKDG 17
XX
XX
XX RESULT 11
XX AAR94778
XX ID AAR94778 standard; peptide; 16 AA.
XX
XX AC AAR94778;
XX
XX DT 11-NOV-1996 (first entry)
XX
XX DE Peptide from library spanning whole of hsp65.
XX
XX KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX KW prophylaxis.
XX
XX OS Synthetic.
XX
XX PN WO9610039-A1.
XX
XX PD 04-APR-1996.
XX
XX PF 27-SEP-1995; 95WO-GB02295.
XX
XX PR 27-SEP-1994; 94GB-0019553.
XX
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX PI Elson CJ, Thompson SJ;
XX
XX WPI: 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX PS
XX CC AAR94773-R94878 are overlapping peptides of a library spanning the
XX CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX CC prepared from the library and used to immunise mice, after 10 days the
XX CC mice received injections of pristane to induce arthritis and the
XX CC animals examined for incidence of arthritis. A preferred anti-arthritis
XX CC peptide was found to correspond to residues 21-31 of full length hsp65
XX CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX CC diseases such as rheumatoid arthritis.
XX
XX Sequence 16 AA;
XX
XX Query Match 46.7%; Score 57; DB 17; Length 16;
XX Best Local Similarity 100.0%; Pred. No. 0.012;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 08-MAR-2001.
 PD
 XX
 PF 30-AUG-2000; 2000WO-1B01326.
 XX
 PR 30-AUG-1999; 99US-0151396.
 XX
 PA (KIES/) KIESSLING R.
 PA (CHAR/) CHARO J M.
 PA (OTEN/) OTENHOFF T H M.
 PA (GELU/) GELUK A.
 XX
 PI KieSSLing R, Charo JM, Otenhoff THM, Geluk A;
 XX
 DR WPI: 2001-244396/25.
 XX
 PT Novel polypeptides containing epitopes derived from Mycobacterial heat
 PT shock protein 65 useful for treating bacterial and parasitic
 PT infections, such as tuberculosis

Disclosure: Page 55; 117pp; English.

CC The present sequence is a peptide epitope derived from Mycobacterial heat
 CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
 CC T-cell (CTL) response in vitro for an infectious microbe e.g.
 CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
 CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
 CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminatium; M. leprae;
 CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
 CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
 CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;
 CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
 CC is useful for treating bacterial and parasitic infections such as
 CC tuberculosis.

XX
 SQ Sequence 10 AA;

Query Match

Best Local Similarity 35.2%; Score 43; DB 22; Length 10;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 8

DB 3 GPKGRNV 10

RESULT 15

91037

AAP91037 standard: peptide; 20 AA.

AC AAP91037;

DT 12-DEC-1989 (first entry)

DE Amino acids 1021-1040 of tetanus toxin.

KW Tetanus toxin fragments; immunogenic conjugates; autoimmune disease;
 cancer; meningitis; T-cell epitope; toxins.

PN W08906974-A.

PD 10-AUG-1989.

PF 31-JAN-1989; 89WO-US00388.

PR 01-FEB-1988; 88US-0150688.

PA (PRAX) PRAXIS BIOLOGICS INC.

PI Bixler G, Pillai S, Insel R;

DR WPI: 1989-24886/34.

PT New isolated and synthetic T-cell bacterial epitope(s)
 PT - used as carriers for antigens, producing immunogenic
 PT conjugates for vaccines.

PS Claim 21: page 86; 103pp; English.

CC Amino acids 1021-1040 of tetanus toxin contg. T-cell
 CC epitope, for use, in conjugates (joined to an antigen
 CC or B-cell epitope) as vaccines. See AAP91043, and AAP90181 for
 CC diptheria conjugates.

XX
 SQ Sequence 20 AA;

Query Match

Best Local Similarity 34.4%; Score 42; DB 10; Length 20;

Matches 9; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 6 NVVLEKKMGAPRTTND 21

DB 4 NAVLANKWVFRTTND 19

Search completed: October 17, 2002, 17:37:56
 job time : 31 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:35:42 ; Search time 14 Seconds
(without alignments)
150,998 Million cell updates/sec

Title: US-09-847-637B-1
Perfect score: 122
Sequence: 1 GPKGRNVLEKKMGAPITTDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
a1 number of hits satisfying chosen parameters: 4259

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	24.6	18	1	MTDFBC
2	29	23.8	17	2	A37823
3	28	23.0	21	2	S03986
4	28	23.0	22	2	A45913
5	27	22.1	18	1	MTMOB
6	27	22.1	21	2	A42762
7	27	22.1	21	2	S62893
8	27	22.1	22	2	A17845
9	26	21.3	14	2	I54945
10	26	21.3	15	2	PH1631
11	26	21.3	16	2	E38501
12	26	21.3	17	2	E53113
13	26	21.3	19	2	PX0062
14	25	20.5	13	1	MTMOB
15	25	20.5	13	1	MTMOB
16	25	20.5	17	2	S03531
17	25	20.5	18	1	DRUFPD
18	25	20.5	18	2	A29558
19	25	20.5	20	2	S46488
20	25	20.5	21	2	S33287
21	25	20.5	21	2	PC1310
22	24.5	20.1	17	2	PH1357
23	24	19.7	15	2	JM0730
24	24	19.7	20	2	PQ0071
25	24	19.7	21	2	I54268
26	23.5	19.3	20	2	S29635
27	23	18.9	11	2	A34243
28	23	18.9	15	2	PH0760
29	23	18.9	22	2	UC0009

30	23	18.9	22	2	A28563
31	22.5	18.4	20	2	F42762
32	22.5	18.4	20	2	PH1380
33	22	18.0	8	2	A31570
34	22	18.0	13	2	G83988
35	22	18.0	17	2	S77834
36	22	18.0	18	2	G84114
37	22	18.0	20	2	S29636
38	22	18.0	20	2	S10876
39	22	18.0	21	2	S71602
40	22	18.0	22	2	P00070
41	21.5	17.6	17	2	S24570
42	21.5	17.6	20	2	S03987
43	21	17.2	11	2	S09074
44	21	17.2	11	2	YHRT
45	21	17.2	11	2	YHRT

ALIGNMENTS

RESULT 1
MTDFBC
melanotropin beta - smaller spotted catshark
C:Species: Scyllorhinus canicula (smaller spotted catshark, smaller spotted dogfish)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01470
R:Love, R.M.; Pickering, B.T.
Gen. Comp. Endocrinol. 24, 398-404, 1974
A:Title: A beta-MSH in the pituitary gland of the spotted dogfish (Scyllorhinus canicula)
A:Reference number: A01470; MUID:75113445
A:Accession: A01470
A:Molecule type: protein
A:Residues: 1-18 <LOV>
C:Superfamily: corticotropin-lipotropin
C:Keywords: hormone

Query Match
Best Local Similarity 24.6%; Score 30; DB 1; Length 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 12 KMGAP 16
DB 11 KMGAP 15

RESULT 2
A37823
dihydroliipoamide S-acetyltransferase (EC 2.3.1.12) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Apr-1991 #sequence_revision 30-Apr-1991 #text_change 05-May-2000
C:Accession: A37823
R:Rahmatullah, M.; Radke, G.A.; Andrews, P.C.; Roche, T.E.
J. Biol. Chem. 265, 14512-14517, 1990
A:Title: Changes in the core of the mammalian-pyruvate dehydrogenase complex upon sel
A:Reference number: A37823; MUID:90354445
A:Accession: A37823
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <RAH>
C:Keywords: acyltransferase; coenzyme A

Query Match
Best Local Similarity 23.8%; Score 29; DB 2; Length 17;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGR 5
DB 1 GPKGR 5
RESULT 3
S03986

agglutinin beta-1 chain - Osage orange
C:Species: Maclura pomifera (Osage orange)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 01-Aug-1997
C:Accession: S03986; S03988
R:Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.
Arch. Biochem. Biophys. 270, 596-603, 1989
A:Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia and M
A:Reference number: S03983; MUID:89206218
A:Accession: S03986
A:Molecule type: protein
A:Residues: 1-21 <Y0U>
A:Note: beta-1 form
A:Accession: S03988
A:Molecule type: protein
A:Residues: 2-21 <Y0Z>
A:Note: beta-3 form

Query Match 23.0%; Score 28; DB 2; Length 21;
Best Local Similarity 33.3%; Pred. No. 9.3e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

1 GPKGRN-VYLEKKWGAPTTN 20
|||:::|||||
2 GPKGKSQSIIVGFWG-DRVTN 21

RESULT 4
A45913
Plantaricin A - Lactobacillus plantarum
C:Species: Lactobacillus plantarum
C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 12-Sep-1997
C:Accession: A45913
R:Nissen-Meyer, J.; Granly-Larsen, A.; Sletten, K.; Daeschel, M.; Nes, I.F.
submitted to the Protein Sequence Database, April 1993
A:Reference number: A45913
A:Accession: A45913
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-22 <N1S>
C:Keywords: antibiotic; bacteriocin

Query Match 23.0%; Score 28; DB 2; Length 22;
Best Local Similarity 83.3%; Pred. No. 9.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

9 LEKKWG 14
| ||||
17 LEKKWG 22

RESULT 5
MT10B
melanotropin beta - horse
C:Species: Equus caballus (domestic horse)
C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
C:Accession: A01467
R:Dixon, J.S.; Li, C.H.
Gen. Comp. Endocrinol. 1, 161-169, 1961
A:Title: The isolation and structure of beta-melanocyte-stimulating hormone from horse F
A:Reference number: A01467
A:Accession: A01467
A:Molecule type: protein
A:Residues: 1-18 <D1X>
C:Superfamily: corticotropin-lipotropin
C:Keywords: hormone

Query Match 22.1%; Score 27; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

12 KMGAP 16
: |||:
11 RWGSS-15

RESULT 6
A42762
multicatalytic endopeptidase complex (EC 3.4.99.46) subunit 13 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
C:Accession: A42762
R:Dick, L.R.; Mooney, C.R.; Pramanik, B.C.; DeMartino, G.N.; Slaughter, C.A.
Biochemistry 31, 7347-7355, 1992
A:Title: Identification and localization of a cysteinyl residue critical for the tryp
A:Reference number: A42762; MUID:92378961
A:Accession: A42762
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-21 <D1C>
A:Note: sequence extracted from NCBI backbone (NCBIP:112172)
C:Superfamily: multicatalytic endopeptidase complex chain C9
C:Keywords: hydrolase

Query Match 22.1%; Score 27; DB 2; Length 21;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

14 GAPTTND 21
| | | | |
8 GCPMTD 15

RESULT 7
S62893
cold-inducible protein, 70K - rainbow trout (fragment)
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 24-Jul-1997
C:Accession: S62893
R:Iamashita, M.; Ojima, N.; Sakamoto, T.
FEBS Lett. 382, 261-264, 1996
A:Title: Induction of proteins in response to cold acclimation of rainbow trout cells
A:Reference number: S62893; MUID:96184500
A:Accession: S62893
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-21 <YAM>

Query Match 22.1%; Score 27; DB 2; Length 21;
Best Local Similarity 46.7%; Pred. No. 1.3e+03;
Matches 7; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

1 GPKGRNVLEKKWGA 15
|||:::|||||
6 GPPGTGKML-IWGA 18

RESULT 8
A12846
hypothetical protein Atu2202 [imported] - Agrobacterium tumefaciens (strain C58, Dupo
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: A12846
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo
erage, G.; Gillet, W.; Grant, C.; Genthner, D.; Kutyavin, T.; Levy, R.; Li, M.; MCI
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Teo, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: A82577; PMID:11743193
A:Accession: A12846
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-22 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAL43191.1; PID:g17740671; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:29:47 : Search time 10 Seconds
(without alignments)
85.183 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122
Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

al number of hits satisfying chosen parameters: 1266

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	25.4	19	1	CH10_CLOPA
2	30	24.6	18	1	MLB_SCYCA
3	28	23.0	20	1	LEC3_MACPO
4	28	23.0	21	1	LEC1_MACPO
5	27	22.1	17	1	FLA2_BARBA
6	27	22.1	18	1	MLB_HORSE
7	25.5	20.9	15	1	LCK_DROME
8	25	20.5	13	1	MLA_CAMDR
9	25	20.5	13	1	MLA_CAMDR
10	25	20.5	15	1	UNO1_PINPS
11	25	20.5	18	1	DRPH_UCAPU
12	24	19.7	21	1	LEC2_ARTIN
13	23	18.9	20	1	LEC1_ARTIN
14	23	18.9	22	1	HGL2_FASHE
15	23	18.9	22	1	PA2_DABRU
16	22	18.0	8	1	ACI_THUAL
17	22	18.0	10	1	UHA3_HUMAN
18	22	18.0	20	1	LEC3_ARTIN
19	22	18.0	22	1	TL11_SPTOL
20	21.5	17.6	11	1	LEC2_MACPO
21	21	17.2	20	1	VR90_BORPE
22	21	17.2	21	1	SCIB_BPTS
23	21	17.2	21	1	SCIB_BPTS
24	20	16.4	13	1	LIGA_TRAVE
25	20	16.4	13	1	UNO2_PINPS
26	20	16.4	16	1	MLB_SCYCA
27	20	16.4	18	1	AGI_EUPMA
28	20	16.4	20	1	PGK_BACCE
29	20	16.4	20	1	TRX_CLOPA
30	19	15.6	9	1	TKIL_LOCMT
31	19	15.6	10	1	BPP2_BOTJA
32	19	15.6	11	1	CEP1_ACHFU
33	19	15.6	12	1	UP01_CAEBL

34	19	15.6	13	1	IDHP_RAT
35	19	15.6	13	1	LIGA_TRAVE
36	19	15.6	14	1	SAP2_ARBP
37	19	15.6	15	1	UC06_MAIZE
38	19	15.6	16	1	MPX_SOLTU
39	19	15.6	18	1	AGI_EUPMA
40	19	15.6	20	1	PGK_CLOPA
41	19	15.6	20	1	YOAH_KLEAE
42	19	15.6	21	1	NEPH_RAT
43	19	15.6	21	1	ODP2_SOLTU
44	18	14.8	9	1	CONO_CONGE
45	18	14.8	10	1	BPP2_BOTIN

ALIGNMENTS

RESULT 1	CH10_CLOPA	STANDARD:	PRT:	19 AA.
ID	CH10_CLOPA			
AC	P81338:			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	10 kDa chaperonin (Protein Cpn10) (GROS protein) (CP 31) (Fragment).			
GN	GROS OR GROS.			
OS	Clostridium pasteurianum.			
OC	Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;			
OC	Clostridium.			
OX	NCBI_TaxID=1501;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-H5;			
RX	MEDLINE=98291870; PubMed=9629918;			
RA	Flengsrud R., Skjeldal L.;			
RT	"Two-dimensional gel electrophoresis separation and N-terminal			
RL	sequence analysis of proteins from Clostridium pasteurianum W5.";			
CC	Electrophoresis 19:802-806(1998).			
CC	-1- FUNCTION: BINDS TO CPN60 IN THE PRESENCE OF MG-ATP AND SUPPRESSES			
CC	THE ATPASE ACTIVITY OF THE LATTER (BY SIMILARITY).			
CC	-1- SUBUNIT: HEPTAMER OF 7 SUBUNITS ARRANGED IN A RING			
CC	(BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE GROS CHAPERONIN FAMILY.			
DR	Interpro: IPR001476: Cpn10.			
DR	Pfam: PF00166: cpn10.1.			
DR	PROSITE: PS00681: CHAPERONINS_CPN10; PARTIAL.			
FT	NON_TER			
FT	SEQUENCE	19 AA; 2026 MW; 7D6B9BD414E60A60 CRC64;		
QY	2 GPKGRNVLEK 11			
Db	5 PLGDNVYIKK 14			
Query Match	Best Local Similarity	25.4%; Score 31; DB 1; Length 19;		
Matches	6; Conservative	Pred. No. 1.7e+02;		
		Mismatches 2; Indels 0; Gaps 0;		
RESULT 2	MLB_SCYCA	STANDARD:	PRT:	18 AA.
ID	MLB_SCYCA			
AC	P01206:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Melanotrophi beta (Beta-MSH).			
OS	Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;			
OC	Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;			
OC	Scyllorhinidae; Scyllorhinus.			
OX	NCBI_TaxID=7830;			
RN	[1]			

```

RP SEQUENCE.
RX MEDLINE-75113445; PubMed-4452470;
RA Love R.M., Pickering B.T.;
RT "A beta-MSH in the pituitary gland of the spotted dogfish
RT (Scyliorhinus canicula): isolation and structure.";
RL Gen. Comp. Endocrinol. 24:398-404(1974).
CC -I- SIMILARITY: BELONGS TO THE POMC FAMILY.
DR PIR: A01470; MTDFEC.
KW Hormone.
SQ SEQUENCE 18 AA; 2195 MW; 353C93A30C314DF4 CRC64;

Query Match 24.6%; Score 30; DB 1; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 KMGAP 16
DB 11 KMGAP 15

RESULT 3
MACPO
ID LEC3_MACPO STANDARD; PRT; 20 AA.
AC P18677;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Agglutinin beta-3 chain (MPA).
OS Maciura pomifera (Osage orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; core eudicots; Rosidae;
OC eucosids I; Rosales; Moraceae; Maciura.
OX NCBI_TaxID-3496;
RN [1]
RP SEQUENCE.
RC TISSUE-Seed;
RX MEDLINE-89206218; PubMed-2705782;
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT "Homology of the D-galactose-specific lectins from Artocarpus
RT integrifolia and Maciura pomifera and the role of an unusual small
RT polypeptide subunit.";
RL Arch. Biochem. Biophys. 270:596-603(1989).
CC -I- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC STRUCTURE GAL-BETAL-3-GALNAC.
CC -I- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -I- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR PIR: S03986; S03988.
DR HSSP: P18676; LJOT.
KW Lectin.
SQ SEQUENCE 20 AA; 2082 MW; AA38811BBD6370E0 CRC64;

Query Match 23.0%; Score 28; DB 1; Length 20;
Best Local Similarity 33.3%; Pred. No. 4.9e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VVLEKKMGAPITN 20
DB 1 GPKGRSOSIIVGPMG-DRVTN 20

RESULT 4
LEC1_MACPO STANDARD; PRT; 21 AA.
AC P18675;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE Agglutinin beta-1 chain (MPA).
OS Maciura pomifera (Osage orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliopsida; core eudicots; Rosidae;
OC eucosids I; Rosales; Moraceae; Maciura.
OX NCBI_TaxID-3496;

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```

RN [1]
RP SEQUENCE.
RC TISSUE-Seed;
RX MEDLINE-89206218; PubMed-2705782;
RA Young N.M., Johnston R.A.Z., Szabo A.G., Watson D.C.;
RT "Homology of the D-galactose-specific lectins from Artocarpus
RT integrifolia and Maciura pomifera and the role of an unusual small
RT polypeptide subunit.";
RL Arch. Biochem. Biophys. 270:596-603(1989).
CC -I- FUNCTION: D-GALACTOSE-SPECIFIC LECTIN, BINDS THE T-ANTIGEN
CC STRUCTURE GAL-BETAL-3-GALNAC.
CC -I- SUBUNIT: FORMED OF FOUR ALPHA CHAINS AND FOUR BETA CHAINS.
CC -I- SIMILARITY: TO THE OTHER AGGLUTININ BETA CHAINS.
DR PIR: S03986; S03986.
DR HSSP: P18676; LJOT.
KW Lectin.
SQ SEQUENCE 21 AA; 2196 MW; AA38811BC1BFD0E0 CRC64;

Query Match 23.0%; Score 28; DB 1; Length 21;
Best Local Similarity 33.3%; Pred. No. 5.1e+02;
Matches 7; Conservative 5; Mismatches 7; Indels 2; Gaps 2;

QY 1 GPKGRN-VVLEKKMGAPITN 20
DB 2 GPKGRSOSIIVGPMG-DRVTN 21

RESULT 5
FLA2_BARBA
ID FLA2_BARBA STANDARD; PRT; 17 AA.
AC P35634;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Flagellin (Fragment).
OS Bartonella bacilliformis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bartonellaceae; Bartonella.
OX NCBI_TaxID-774;
RN [1]
RP SEQUENCE.
RC STRAIN-KC584;
RX MEDLINE-94041612; PubMed-8225570;
RA Scherer D.C., Deburon-Connors I., Minnick M.F.;
RT "Characterization of Bartonella bacilliformis flagella and effect of
RT anti-flagellin antibodies on invasion of human erythrocytes.";
RL Infect. Immun. 61:4962-4971(1993).
CC -I- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES TO
CC FORM THE FILAMENTS OF BACTERIAL FLAGELLA. FLAGELLA ARE AN
CC IMPORTANT COMPONENT IN THE INVASIVENESS OF B.BACILLIFORMIS.
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
KW Flagella.
SQ SEQUENCE 17 AA; 1746 MW; BA24EB6177FCD8C8 CRC64;

Query Match 22.1%; Score 27; DB 1; Length 17;
Best Local Similarity 62.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 GAPITND 21
DB 1 GAAILTND 8

RESULT 6
MLB_HORSE
ID MLB_HORSE STANDARD; PRT; 18 AA.
AC P01202;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Melanotropin beta (Beta-MSH).
OS Equus caballus (Horse).

```


GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:30:22 : Search time 24 Seconds
(without alignments)
158.579 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122

Sequence: 1 GPKGRNVLEKKMGAPITINDG 22

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

a1 number of hits satisfying chosen parameters: 6912

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	28.7	18	6	Q9TRD8
2	27.5	22.5	16	4	Q9UCK9
3	27	22.1	17	4	Q9UPK4
4	27	22.1	21	13	Q9PRQ1
5	27	22.1	22	2	Q9AH71
6	27	22.1	22	13	Q9PRM2
7	26	21.3	14	2	Q47599
8	26	21.3	17	2	Q9R512
9	26	21.3	18	15	Q73920
10	25	20.5	18	15	Q73921
11	25	20.5	10	11	Q70580
12	25	20.5	15	9	Q38427
13	25	20.5	16	2	Q45530
14	25	20.5	17	4	Q9UC91
15	25	20.5	19	13	Q9PRM4
16	20.5	20.5	20	13	Q9PRM3

17	25	20.5	20	15	Q73917
18	25	20.5	20	15	Q73918
19	25	20.5	21	5	Q9AJG0
20	25	20.5	21	5	Q9TW05
21	25	20.5	22	11	Q9QWB6
22	25	20.5	22	13	Q910C6
23	25	20.5	22	13	Q902V4
24	25	20.5	22	13	Q902V3
25	25	20.5	22	13	Q902V2
26	24	19.7	10	4	Q9UNF2
27	24	19.7	11	4	Q60842
28	24	19.7	15	2	Q9R4P5
29	24	19.7	17	6	Q29395
30	24	19.7	18	6	Q9N1D5
31	24	19.7	18	15	Q73487
32	24	19.7	20	1	Q9UWM8
33	24	19.7	21	4	Q15965
34	24	19.7	22	1	Q9UW19
35	23.5	19.3	20	10	Q9S8T1
36	23	18.9	11	2	P83147
37	23	18.9	11	15	Q83410
38	23	18.9	13	15	Q85645
39	23	18.9	16	2	Q10748
40	23	18.9	16	4	Q9UC18
41	23	18.9	16	8	Q9T2V8
42	23	18.9	16	10	Q9S8D6
43	23	18.9	17	4	Q9UCF0
44	23	18.9	17	8	Q03888
45	23	18.9	17	15	Q73442

ALIGNMENTS

RESULT 1					
Q9TRD8	PRELIMINARY:	PRT:	18 AA.		
Q9TRD8	Q9TRD8				
AC	Q9TRD8				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2000 (TREMBLrel. 14, Last annotation update)				
DE	CHAPERONIN (FRAGMENT).				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
OX	NCBI_TaxID=9986;				
RM	[1]				
RP	SEQUENCE.				
RX	MEDLINE=94089752; PubMed=7903455;				
RA	Rommelare H., Van Troye M., Gao Y., Melki R., Cowan N.J.,				
RA	Vandekerckhove J., Ampe C.;				
RT	"Eukaryotic cytosolic chaperonin contains t-complex polypeptide 1 and				
RT	seven related subunits.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 90:11975-11979(1993).				
SO	SEQUENCE 18 AA; 1884 MW; B608F6EBB5A2A26 CRC64;				
Query Match	28.7%;	Score 35;	DB 6;	Length 18;	
Best Local Similarity	46.7%;	Pred. No. 1;	le=02;		
Matches	7;	Conservative	3;	Mismatches	5;
				Indels	0;
				Gaps	0;
QY	8 VLEKKMGAPITINDG 22				
DB	1 MMTDKGDVTVINDG 15				
RESULT 2					
Q9UCK9	PRELIMINARY:	PRT:	16 AA.		
AC	Q9UCK9				
DT	01-MAY-2000 (TREMBLrel. 13, Created)				
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)				
DE	SERUM AMYLOID A ISOTYPE 2 ALPHA PROTEIN (FRAGMENT).				

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
[1]
RM
RN
RP
RQ MEDLINE=30099171; PubMed=1463770;
RX Babu S., Takahashi T., Kasama T., Shirasawa H.,
RA "Identification of two novel amyloid A protein subsets coexisting in
RT an individual patient of AA-amyloidosis.",
RL Biochim. Biophys. Acta 1180:195-200(1992).
DR Interpro: IPR000096; Setum_amyloid_A.
DR Pfam: PF00277; SAA_proteins; 1.
SQ
SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9CBCC1 CRC64;

Query Match	22.5%;	Score 27.5;	DB 4;	Length 16;
Best Local Similarity	35.0%;	Pred. NO. 1.5e+03;		
Matches	7;	Conservative	1;	Mismatches 5;
			Indels 7;	Gaps 1

1 GPKGRNVLEKKWGAPTITN 20
2 GPGG-----AMAAEVISN 14

RESULT 3	
Q9UPK4	
ID Q9UPK4	PRELIMINARY;
	PRT; 17 AA

DT	01-MAY-2000 (Tremblrel, 13, Created)
DT	01-MAY-2000 (Tremblrel, 13, last sequence update)
DT	01-MAY-2000 (Tremblrel, 13, last annotation update)

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
0X NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McGready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Dangnan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Traanheim M., Amico-Keller G.,
RA Coesfeld J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Kronmüller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Koyashashi A., Olsen A.S., Garrano A.V.
RT "Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a
serine protease gene cluster." submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

FT	NON_TER	17	17
SO	SEQUENCE	17 AA;	2166 MW; B73A34E7EDB2DE5D CRC64;

Query Match	22.1%;	Score 27;	DB 4;	Length 17;
Best Local Similarity	46.2%;	Pred. NO. 1.9e+03;		
Matches	6;	Conservative	2;	Mismatches 3;
			Indels 2;	Gaps 1;

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Qy 1 GPKGRNVLEKKW 13
    ||:|:| |
Db 7 GPRYRELV--KNW 17
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RESULT 4	
Q9PRQ1	
ID Q9PRQ1	PRELIMINARY;
	PRT; 21 AA.

DT 01-MAY-2000 (TREMBLER, 13, Created)
DT 01-MAY-2000 (TREMBLER, 13, last sequence update)
DT 01-MAY-2000 (TREMBLER, 13, last annotation update)
DE 70 KDa COLD ACCLIMATION-RELATED PROTEIN (FRAGMENT).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protaetnophlebotrym, Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RM [1]
RP SEQUENCE:
RX MEDLINE=96184500; PubMed=8605981;
RA Yamashita M., Ojima N., Sakamoto T.,
RT "Induction of proteins in response to cold acclimation of rainbow
trout cells.";
RL FEBS Lett. 382:261-264(1996).
SQ SEQUENCE 21 AA; 2129 MW; FF6BD74564917510 CRC64;

Query Match	22.1%;	Score 27;	DB 13;	length 21;
Best Local	Similarity	46.7%;	Pred. No. 2.4e+03;	
Matches	7; Conservative	1;	Mismatches 5;	Indels 2; Gaps 1.

```
QY      1 GPKGRNVLEKKWGA 15
        ||| :|| |||
Db      6 GPPGTGKML--IWGA 18
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RESULT 5	
Q9AH71	
ID Q9AH71	PRELIMINARY; PRT; 22 AA

DT	01-JUN-2001	(TREMBlrel. 17, Created)
DT	01-JUN-2001	(TREMBlrel. 17, Last sequence update)
DT	01-DEC-2001	(TREMBlrel. 19, Last annotation update)

GN HMBR.
OS *Neisseria meningitidis*.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.

SEQUENCE FROM N.A
STRAIN=44/76;
MEDLINE=21116988;
RX

RX MEDLINE:21116988; PubMed-11779344;
RA Kahler C.M., Blum E., Miller Y.K., Ryan D., Popovic T., Stephens D.S.: "The
RT "x1, an exchangeable genetic island in *Neisseria meningitidis*,"
RL Infect. Immun. 69:1687-1696(2001).
DR EMBL: AF319527; AAK8019.1; -;
DR InterPro: IPR000531; TonB_boxC.

```

ON      FNAME, FILENO, LONG_DESC, 1,
FT      NON_TER      1      1
SQ      SEQUENCE      22 AA; 2584 MN; F1BEB6F2F3C2C49 CRC64;

```

Query Match	22.1%	Score 27	DB 2	Length 22
Best Local Similarity	40.0%	Pred. No. 2.5e+03		
Matches 4, Conservative		2	Mismatches 4	Indels 0
				Gaps 0

QY	4	GRNVLEKKW	13
		:	!
Db	11	GRNYAVSLEW	20

RESULT 6	
Q9PRN2	
ID Q9PRN2	PRELIMINARY;
	PRT; 22 AA

DT	01-MAY-2000 (Tremblrel. 13, last sequence update)
DT	01-MAY-2000 (Tremblrel. 13, last annotation update)
DE	CORTICOTROPIN, ACTH.

0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia,
0C Petromyzontiformes; Petromyzontidae; Petromyzon.
0X NCBI_TaxID=7757;

RP SEQUENCE.
RX MEDLINE=6122167; PubMed=8537171;
RA Takahashi A., Amemiya Y., Nozaki M., Sower S.A., Joss J., Gorman A.

RT "Isolation and characterization of melanotropins from lamprey
RT pituitary glands."; RT

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:37:27 : Search time 13 seconds

(without alignments)
41.336 Million cell updates/sec

Title: US-09-847-637B-1

Perfect score: 122
Sequence: 1 GPKGRNVLEKKWCAPIRTNDG 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

127829

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

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5: /cgn2_6/ptodata/1/1aa/PTCIV.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	29.5	8	2	US-08-467-822-11
2	36	29.5	8	4	US-08-432-697-11
3	36	29.5	8	4	US-08-466-248-11
4	35	28.7	18	1	US-08-204-487-4
5	35	28.7	20	1	US-07-755-161A-1
6	35	28.7	20	1	US-07-755-161A-2
7	35	28.7	20	1	US-07-891-174-1
8	35	28.7	20	1	US-07-891-174-2
9	35	28.7	20	1	US-08-204-487-2
10	35	28.7	20	1	US-08-256-771-22
11	35	28.7	20	1	US-08-256-771-23
12	35	28.7	20	1	US-08-381-984-22
13	35	28.7	20	1	US-08-381-984-23
14	34	27.9	17	4	US-08-996-679-63
15	34	27.9	17	4	US-08-939-853A-14
16	34	27.9	17	4	US-09-115-395-23
17	34	27.9	17	4	US-09-113-977C-68
18	34	27.9	17	4	US-09-250-059-54
19	34	27.9	17	4	US-09-248-074-54
20	34	27.9	17	4	US-09-187-859-50
21	33.5	27.5	20	3	US-08-614-935-10
22	33.5	27.5	20	3	US-09-130-287-10
23	32	26.2	10	4	US-08-687-590-67
24	31	25.4	20	1	US-08-440-861-50
25	30	24.6	14	4	US-08-584-043A-60
26	30	24.6	16	4	US-08-602-999A-228
27	30	24.6	16	4	US-08-030-410-1

28	30	24.6	17	1	US-07-838-410-4	Sequence 4, Appl1
29	30	24.6	20	1	US-08-483-115-2	Sequence 2, Appl1
30	30	24.6	21	4	US-08-584-043A-81	Sequence 81, Appl
31	29.5	24.2	18	2	US-08-845-926-32	Sequence 32, Appl
32	29.5	24.2	20	2	US-08-617-929-8	Sequence 8, Appl1
33	29.5	24.2	20	2	US-08-617-929-12	Sequence 12, Appl1
34	29	23.8	13	5	PCT-US95-07543-3	Sequence 3, Appl1
35	29	23.8	20	3	US-08-256-747C-7	Sequence 7, Appl1
36	29	23.8	20	4	US-08-834-130A-7	Sequence 7, Appl1
37	28	23.0	16	1	US-08-300-386A-38	Sequence 38, Appl
38	28	23.0	16	3	US-08-931-645-38	Sequence 38, Appl
39	28	23.0	16	5	PCT-US94-01258-38	Sequence 38, Appl
40	28	23.0	16	5	PCT-US95-11235-38	Sequence 38, Appl
41	28	23.0	17	4	US-09-227-357-406	Sequence 406, App
42	28	23.0	18	3	US-08-336-553A-52	Sequence 52, Appl
43	28	23.0	18	4	US-09-128-344A-31	Sequence 31, Appl
44	28	23.0	18	4	US-09-128-344A-114	Sequence 114, App
45	28	23.0	18	4	US-09-128-344A-135	Sequence 135, App

ALIGNMENTS

RESULT 1
US-08-467-822-11
Sequence 11, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flimegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-822-11

Query Match 29.5%; Score 36; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 7
11:11111
DB 2 GPKGRNV 8

RESULT 2
US-08-432-697-11
Sequence 11, Application US/08432697
Patent No. 6248330

GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995

CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-432-697-11

Query Match 29.5%; Score 36; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 7
11:11111
DB 2 GPKGRNV 8

RESULT 3
US-08-466-248-11
Sequence 11, Application US/08466248

Patent No. 6258359
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thibierge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995

ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-248-11

Query Match 29.5%; Score 36; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 7
11:11111
DB 2 GPKGRNV 8

RESULT 4
US-08-204-487-4
Sequence 4, Application US/08204487
Patent No. 5565425

GENERAL INFORMATION:

APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIYAKI

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:38:52 ; Search time 25 Seconds
(without alignments)
71.087 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90
Sequence: 1 GPKGRNVYLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

al number of hits satisfying chosen parameters: 200626

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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5: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	90	100.0	16	21	AAV93329
2	83	92.2	15	17	AAV94779
3	83	92.2	15	18	AAW43457
4	61	67.8	16	17	AAV94780
5	61	67.8	16	18	AAW43458
6	57	63.3	16	17	AAV94778
7	57	63.3	16	18	AAW43456
8	55	61.1	16	21	AAV93330
9	47	52.2	11	22	AAV88272
10	43	47.8	10	22	AAV88269
11	39	43.3	9	22	AAV88279

12	38	42.2	15	17	AAV94781
13	38	42.2	15	18	AAW43459
14	34	37.8	14	21	AAV10751
15	34	37.8	14	21	AAV10751
16	34	37.8	14	22	AAV35931
17	34	37.8	15	22	AAV64099
18	31	34.4	10	22	AAV90858
19	30	33.3	10	21	AAV32456
20	30	33.3	14	18	AAV36766
21	30	33.3	14	18	AAV25443
22	30	33.3	15	19	AAV37382
23	29.5	32.8	15	19	AAV45892
24	29	32.2	9	22	AAV88962
25	29	32.2	13	17	AAV88962
26	29	32.2	13	18	AAV19794
27	29	32.2	14	22	AAV97155
28	29	32.2	14	22	AAV00717
29	29	32.2	15	19	AAV75543
30	28.5	31.7	10	22	AAV94842
31	28	31.1	9	19	AAV56753
32	28	31.1	9	22	AAV02332
33	28	31.1	12	18	AAV38002
34	28	31.1	13	21	AAV57009
35	28	31.1	13	21	AAV57010
36	28	31.1	14	22	AAV98555
37	28	31.1	14	22	AAV00664
38	28	31.1	15	18	AAV36770
39	28	31.1	15	22	AAV68351
40	28	31.1	16	15	AAV58521
41	28	31.1	16	17	AAV95294
42	28	31.1	16	21	AAV39000
43	27.5	30.6	16	19	AAV69100
44	27	30.0	7	22	AAV44111
45	27	30.0	7	22	AAV46151

ALIGNMENTS

RESULT 1
ID AAV93329 standard; peptide: 16 AA.
XX
AC AAV93329;
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
KW Inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200027870-A1.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-IL00595.
XX
PR 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
XX
PI Naparstek Y, Ulanovsky R, Kashi Y;
XX
DR WPI: 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT Immunity against autoimmune disease or inflammatory disorders.
PS Claim 2; Page 7; 58pp; English.

```

XX The present sequence represents an epitope of the heat shock protein
CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
CC nucleic acid encoding it, are useful in vaccines for conferring
CC immunity against autoimmune disease or inflammatory disorders,
CC especially arthritis. The peptide may also be used to raise
CC antibodies, which are then used for passive immunisation.
XX
SQ Sequence 16 AA;

Query Match          100.0%; Score 90; DB 21; Length 16;
Best Local Similarity 100.0%; Pred. No. 8e-09;
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGAP 16
   |||||
DB 1 GPKGRNVLEKKWGAP 16

BUT 2
AAR94779 standard; peptide: 15 AA.
AC AAR94779;
XX
XX 11-NOV-1996 (first entry)
XX
DE Peptide from library spanning whole of hsp65.
XX
XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
XX rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX prophylaxis.
XX
OS Synthetic.
XX
XX WO9610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95WO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI: 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
XX in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-B94878 are overlapping peptides of a library spanning the
XX whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
XX prepared from the library and used to immunise mice, after 10 days the
XX mice received injections of pristane to induce arthritis and the
XX animals examined for incidence of arthritis. A preferred anti-arthritis
XX peptide was found to correspond to residues 21-31 of full length hsp65
XX (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
XX treatment and prophylaxis (may be used in a vaccine) of autoimmune
XX diseases such as rheumatoid arthritis.
XX
SQ Sequence 15 AA;

Query Match          92.2%; Score 83; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
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```

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DB 1 GPKGRNVLEKKWGA 15

RESULT 3
AAM43457
ID AAM43457 standard; peptide: 15 AA.
XX
XX AAM43457;
XX
XX 08-APR-1998 (first entry)
XX
XX Mycobacteria sp. hsp68 derived peptide (group 1 #7).
DE
XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
XX rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
OS Synthetic.
OS Mycobacteria sp.
XX
XX WO9711966-A1.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96WO-GB02382.
XX
XX 27-SEP-1995; 95GB-0019737.
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX Elson CJ, Thompson JS;
XX
XX WPI: 1997-212851/19.
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
XX for treatment of autoimmune disease esp. arthritis
XX
PS Disclosure: Fig 1a; 91pp; English.
XX
XX This peptide is one of a library (see AAM43451-W43556) which represents
XX the mycobacterial heat shock protein, hsp65 and is designed to study
XX a novel method for the treatment of autoimmune disease e.g. Rheumatoid
XX arthritis. This fragment has been allocated as a group 1 peptide which
XX is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
XX hsp65 is known to be an immunodominant antigen in a number of infectious
XX diseases and is linked to pristane induced arthritis (PIA) in vitro.
XX however heat shock proteins and peptides derived from microbial sources
XX may act as self antigens and thus have limited clinical use. The human
XX hsp65 homologue, hsp58, or fragments of the hsp58 protein
XX (see AAM14948-W14950) may be useful in the development of vaccines for
XX prophylaxis or treatment of an autoimmune disease such as rheumatoid
XX arthritis.
XX
SQ Sequence 15 AA;

Query Match          92.2%; Score 83; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e-07;
Matches 15: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEKKWGA 15
   |||||
DB 1 GPKGRNVLEKKWGA 15

RESULT 4
AAR94780
ID AAR94780 standard; peptide: 16 AA.
XX
XX AAR94780;
XX
XX 11-NOV-1996 (first entry)
XX
XX Peptide from library spanning whole of hsp65.
XX

```

XX Hsp: heat shock protein; Mycobacterium bovis: microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KM prophylaxis.
 OS Synthetic.
 XX WO9610039-A1.
 PN 04-APR-1996.
 PD 27-SEP-1995; 95WO-GB02295.
 XX 27-SEP-1994; 94GB-0019553.
 PR (PEPT-) PEPTIDE THERAPEUTICS LTD.
 PA Elson CJ, Thompson SJ;
 XX WPI: 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.

CC Sequence 16 AA;

Query Match 67.8%; Score 61; DB 17; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00088;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVYLEKKMGAP 16
 DB 1 NVYLEKKMGAP 11

● JLT 5
 43458

ID AAW43458 standard; peptide; 16 AA.

XX AAW43458;

AC 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #8).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristane induced arthritis; PIA.

OS Synthetic.

OS Mycobacteria sp.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson SJ;

DR WPI: 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis

PS Disclosure; Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro.
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW14948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

CC Sequence 16 AA;

Query Match 67.8%; Score 61; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.00088;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 NVYLEKKMGAP 16
 DB 1 NVYLEKKMGAP 11

RESULT 6
 AAR94778

ID AAR94778 standard; peptide; 16 AA.

AC AAR94778;

DE 11-NOV-1996 (first entry)

PT Peptide from library spanning whole of hsp65.

KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KM prophylaxis.

OS Synthetic.

PN WO9610039-A1.

PD 04-APR-1996.

PF 27-SEP-1995; 95WO-GB02295.

PR 27-SEP-1994; 94GB-0019553.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;

DR WPI: 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the

CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.

XX
 SQ Sequence 16 AA;

Query Match 63.3%; Score 57; DB 17; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEK 11
 |||||
 DB 6 GPKGRNVLEK 16

AAW43456 standard; peptide; 16 AA.

AAW43456;

08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #6).

KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KM rheumatoid arthritis; antigen; infectious disease; prophylactic;
 XX pristane induced arthritis; PIA.

OS Synthetic.
 OS Mycobacteria sp.

PN WO9711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

XX Elson CJ, Thompson JS;

WI; 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful
 PT for treatment of autoimmune disease esp. arthritis

PS Disclosure: Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAW43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAW1948-W1950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

SQ Sequence 16 AA;

Query Match 63.3%; Score 57; DB 18; Length 16;

Best Local Similarity 100.0%; Pred. No. 0.0043;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNVLEK 11
 |||||
 DB 6 GPKGRNVLEK 16

RESULT 8

ID AAY93330 standard; peptide; 16 AA.

AC AAY93330;

DT 04-SEP-2000 (first entry)

DE Amino acid sequence of an epitope of heat shock protein 60.

KW Epitope; heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 KM inflammatory disorder; arthritis.

OS Mycobacterium tuberculosis.

PN WO20027870-A1.

PD 18-MAY-2000.

PF 04-NOV-1999; 99WO-IL00595.

PR 05-NOV-1998; 98US-0107213.

PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX Naparstek Y, Ulmansky R, Kashi Y;

WI; 2000-376486/32.

PT Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -

PS Claim 3; Page 7; 58pp; English.

CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.

SQ Sequence 16 AA;

Query Match 61.1%; Score 55; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0097;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 VLEKKWGAP 16
 |||||
 DB 1 VLEKKWGAP 10

RESULT 9

ID AAB88272 standard; peptide; 11 AA.

AC AAB88272;

DT 17-MAY-2001 (first entry)

DE Hsp-65 peptide epitope #46.

KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculosstatic;
 KM Immune response inducer; vaccine; gene therapy; bacterial infection;


```

KM tuberculosi.
XX
OS Mycobacterium sp.
XX
PN WO200116174-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-IB01326.
XX
PR 30-AUG-1999; 99US-0151396.
XX
PA (KIES/) KIESSLING R.
PA (CHAR/) CHARO J M.
PA (OTEN/) OTENHOFF T H M.
PA (GELU/) GELUK A.
XX
PI KieSSLing R, Charo JM, Otenhoff THM, Geluk A;
PI WPI: 2001-244396/25.
XX
PT Novel polypeptides containing epitopes derived from Mycobacterial heat
PT shock protein 65 useful for treating bacterial and parasitic
XX infections, such as tuberculosis
XX
PS Disclosure: Page 55; 117pp; English.
XX
CC The present sequence is a peptide epitope derived from Mycobacterial heat
CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
CC T-cell (CTL) response in vitro for an infectious microbe e.g.
CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;
CC M.paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
CC Yersinia enterocolitica; Neisseria meningitidis; N.gonorrhoeae;
CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
CC is useful for treating bacterial and parasitic infections such as
CC tuberculosis.
XX
SQ Sequence 11 AA;
Query Match 52.2%; Score 47; DB 22; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNVVL 9
3 GPKGRNVVL 11
RESULT 10
AAB88269
ID AAB88269 standard; Peptide: 10 AA.
XX
AC AAB88269;
XX
DT 17-MAY-2001 (first entry)
XX
DE Hsp-65 peptide epitope #43.
XX
KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
KW immune response inducer; vaccine; gene therapy; bacterial infection;
KW tuberculosi.
XX
OS Mycobacterium sp.
XX
PN WO200116174-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-IB01326.
XX
PR
XX
PI
XX

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PR 30-AUG-1999; 99US-0151396.
XX
PA (KIES/) KIESSLING R.
PA (CHAR/) CHARO J M.
PA (OTEN/) OTENHOFF T H M.
PA (GELU/) GELUK A.
XX
PI KieSSLing R, Charo JM, Otenhoff THM, Geluk A;
PI WPI: 2001-244396/25.
XX
PT Novel polypeptides containing epitopes derived from Mycobacterial heat
PT shock protein 65 useful for treating bacterial and parasitic
XX infections, such as tuberculosis
XX
PS Disclosure: Page 55; 117pp; English.
XX
CC The present sequence is a peptide epitope derived from Mycobacterial heat
CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
CC T-cell (CTL) response in vitro for an infectious microbe e.g.
CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;
CC M.paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
CC Yersinia enterocolitica; Neisseria meningitidis; N.gonorrhoeae;
CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
CC is useful for treating bacterial and parasitic infections such as
CC tuberculosis.
XX
SQ Sequence 10 AA;
Query Match 47.8%; Score 43; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPKGRNV 8
3 GPKGRNV 10
Db
RESULT 11
AAB88279
ID AAB88279 standard; Peptide: 9 AA.
XX
AC AAB88279;
XX
DT 17-MAY-2001 (first entry)
XX
DE Hsp-65 peptide epitope #53.
XX
KW Heat shock protein-65; hsp-65; epitope; antibacterial; tuberculostatic;
KW immune response inducer; vaccine; gene therapy; bacterial infection;
KW tuberculosi.
XX
OS Mycobacterium sp.
XX
PN WO200116174-A2.
XX
PD 08-MAR-2001.
XX
PF 30-AUG-2000; 2000WO-IB01326.
XX
PR 30-AUG-1999; 99US-0151396.
XX
PA (KIES/) KIESSLING R.
PA (CHAR/) CHARO J M.
PA (OTEN/) OTENHOFF T H M.
PA (GELU/) GELUK A.
XX
PI KieSSLing R, Charo JM, Otenhoff THM, Geluk A;
PI WPI: 2001-244396/25.
XX

```

XX Novel polypeptides containing epitopes derived from Mycobacterial heat
PT shock protein 65 useful for treating bacterial and parasitic
PT infections, such as tuberculosis
XX
PS Disclosure: Page 55; 117pp; English.
XX
XX The present sequence is a peptide epitope derived from Mycobacterial heat
CC shock protein 65. This peptide epitope is useful for inducing a cytotoxic
CC T-cell (CTL) response in vitro for an infectious microbe e.g.
CC Mycobacteria e.g. Mycobacterium tuberculosis; Rickettsia; Chlamydia;
CC Trypanosoma; Helicobacter; Leishmania; Trichomonas e.g. T. vaginalis;
CC Synechococcus e.g. S. vulcanis; Cowdria e.g. C. ruminalium; M. leprae;
CC M. paratuberculosis; Brucella abortus; Leptospira interrogans; Legionella
CC pneumophila; Coxiella burnetii; Staphylococcus aureus; Salmonella typhi;
CC Yersinia enterocolitica; Neisseria meningitidis; N. gonorrhoeae;
CC Haemophilus influenzae and Pseudomonas aeruginosa. This peptide epitope
CC is useful for treating bacterial and parasitic infections such as
tuberculosis.

Sequence 9 AA:
Query Match 43.3%; Score 39; DB 22; Length 9;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKGRNV 7
|||||||
DB 3 GPKGRNV 9

RESULT 12
AAR94781
ID AAR94781 standard; peptide; 15 AA.
XX
AC AAR94781;
XX
DT 11-NOV-1996 (first entry)
XX
DE Peptide from library spanning whole of hsp65.
XX
KW Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KW Rheumatoid arthritis; autoimmune disease; treatment; vaccine;
XX
XX prophylaxis.
OS Synthetic.
XX
XX WO9610039-A1.
XX
XX 04-APR-1996.
XX
XX 27-SEP-1995; 95WO-GB02295.
XX
XX 27-SEP-1994; 94GB-0019553.
XX
XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
XX Elson CJ, Thompson SJ;
XX
XX WPI: 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
XX rheumatoid arthritis.
XX
XX Example 1; Figure 1; 88pp; English.
XX
XX AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC Prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65

CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 15 AA:
Query Match 42.2%; Score 38; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAP 16
|||||||
DB 1 KKWGAP 6

RESULT 13
AAM43459
ID AAM43459 standard; peptide; 15 AA.
XX
AC AAM43459;
XX
DT 08-APR-1998 (first entry)
XX
DE Mycobacteria sp. hsp68 derived peptide (group 1 #9).
XX
KW Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
XX pristane induced arthritis; PIA.
XX
OS Synthetic.
OS Mycobacteria sp.
XX
XX WO9711966-A1.
XX
XX 03-APR-1997.
XX
XX 26-SEP-1996; 96WO-GB02382.
XX
XX 27-SEP-1995; 95GB-0019737.
XX
XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
XX
XX Elson CJ, Thompson JS;
XX
XX WPI: 1997-212851/19.
XX
XX Polypeptide(s) derived from microbial heat shock protein - useful
PT for treatment of autoimmune disease esp. arthritis
XX
PS Disclosure: Fig 1a; 91pp; English.
XX
XX This peptide is one of a library (see AAM43451-W43556) which represents
CC the mycobacterial heat shock protein, hsp65 and is designed to study
CC a novel method for the treatment of autoimmune disease e.g. Rheumatoid
CC arthritis. This fragment has been allocated as a group 1 peptide which
CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
CC hsp65 is known to be an immunodominant antigen in a number of infectious
CC diseases and is linked to pristane induced arthritis (PIA) in vitro.
CC however heat shock proteins and peptides derived from microbial sources
CC may act as self antigens and thus have limited clinical use. The human
CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
CC (see AAM1948-W14950) may be useful in the development of vaccines for
CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
CC arthritis.
XX
XX Sequence 15 AA:
Query Match 42.2%; Score 38; DB 18; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 KKWGAP 16
|||||||

Db 1 KKWGAP 6

RESULT 14

AB010751
ID AAB010751 standard; peptide: 14 AA.XX
AC AAB010751;XX
DT 26-JAN-2001 (first entry)XX
DE Fibrin gel binding peptide SEQ ID NO: 10.XX
KW Fibrin; fibrin gel; neurite extension; neurotrophic.XX
OS Synthetic.XX
PN DE20010297-01.XX
XX 31-AUG-2000.XX
PS 08-JUN-2000; 2000DE-2010297.XX
PR 08-JUN-2000; 2000DE-2010297.XX
PA (ETHZ-) ETH ZUERICH.XX
PA (UZH-) UNIV ZUERICH.XX
DR WPI: 2000-580546/55.XX
PT Protein gel containing mixture of peptides, useful e.g. for stimulatingXX
PS Claim 4; Page 10; 38pp; German.XX
CC This invention describes a novel fibrin (or other protein) gel (A) thatXX
CC includes a mixture of peptides (B), crosslinked with the gel to stimulateXX
CC extension of neurites. The products of the invention have neurotrophicXX
CC activity. (A) are useful for supporting tissues and for cellXX
CC incorporation or growth, especially for stimulating growth and extensionXX
CC of neurites. Many different types of cells can bind to, and grow on (A),XX
CC or related gels or three-dimensional matrices containing them, and theXX
CC three-dimensional structures significantly increase (sometimesXX
CC synergistically) neurite growth and extension. The gels may also includeXX
XX a protease inhibitor to control the rate at which they degrade in vivo.XX
SQ Sequence 14 AA:XX
QY Query MatchXX
ID AAB01586 standard; peptide: 14 AA.XX
AC AAB01586;XX
DT 08-NOV-2000 (first entry)XX
DE Proteoglycan binding domain of neural cell adhesion molecule.XX
KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;XX
KW sealant; tissue engineering; wound healing; scaffold;XX
KW cell transplant; adhesion prevention; cell migration; collagenase;XX
OS plasmid; elastase.XX
PN WO200044808-A1.XX
PD 03-AUG-2000.XX
PF 01-FEB-2000; 2000WO-US02608.XX
PR 01-FEB-1999; 99US-0118093.XX
PA (HUBB/) HUBBELL J A.XX
PI Hubbell JA, Elbert D, Lutolf M, Pratt A, Schoenmakers R;XX
PI Tjellell N, Vernon B;XX
DR WPI: 2000-524289/47.XX
PT Producing polymeric biomaterials by polymerizing two or more precursorXX
PT components (e.g. polymer, protein or peptide) of the biomaterial,XX
PT useful for delivering therapeutic molecules to a subject and asXX
PT adhesives or sealantsXX
PS Disclosure: Page 53; 119pp; English.XX
CC A method of making polymeric biomaterials is described comprisingXX
CC combining two or more precursor components (e.g. polymer, protein orXX
CC peptide) of the biomaterial under conditions that allowXX
CC polymerisation of the two components. Polymerisation occurs throughXX
CC self selective reaction between a strong nucleophile and a conjugatedXX
CC unsaturated bond or a conjugated unsaturated group, by nucleophilicXX
CC addition. The polymeric hydrogels can be used in a variety ofXX
CC applications. They can be used to deliver therapeutic molecules toXX
CC a subject, as adhesives or sealants (e.g. sealing air leaks on theXX
CC lung), as tissue engineering and wound healing scaffolds, and as cellXX
CC transplant devices. The biomaterials are also useful for adhesionXX
CC prevention to minimise unwanted operative or post-traumatic adhesions.XX
CC A variety of adhesion-promoting peptides have been identified asXX
CC being the active domains of adhesion-promoting proteins such asXX
CC fibronectin, vitronectin, laminin, collagen, von Willebrand factorXX
CC osteonectin etc.. These peptides can be incorporated into theXX
CC biomaterial when they are designed with a strong nucleophile in theXX
CC peptide chain such as cysteine. These peptides are potentially usefulXX
CC in controlling a variety of cellular reactions such as cellXX
CC attachment, migration and overgrowth on a material surface when theXX
CC material is non bio-degradable or slowly degradable, and cellXX
CC migration through a material when that material is biodegradable.XX
CC The peptides are also useful in the induction of particular cellularXX
CC phenotypes. The matrix proteins also comprise peptide sequencesXX
SQ which bind to glycoprotein cell surface receptors.XX
SQ Sequence 14 AA:XX
QY Query MatchXX
ID AAB01586 standard; peptide: 14 AA.XX
AC AAB01586;XX
DT 08-NOV-2000 (first entry)XX
DE Proteoglycan binding domain of neural cell adhesion molecule.XX
KW Polymer; biomaterial; conjugate; hydrogel; drug delivery; adhesive;XX
KW sealant; tissue engineering; wound healing; scaffold;XX
KW cell transplant; adhesion prevention; cell migration; collagenase;XX
KW plasmid; elastase.XX
OS Synthetic.Search completed: October 17, 2002, 17:42:56
Job time : 26 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:41:23 : Search time 13 seconds
(without alignments)
118.264 Million cell updates/sec

Title: US-09-847-637B-2

Perfect score: 90

Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

al number of hits satisfying chosen parameters: 2769

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: PIR_71:*
2: pir1:*
3: pir2:*
4: pir3:*
5: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	28.9	14	2	154945 gene C protein - E
2	26	28.9	16	2	ES8501 25K kidney and gal
3	25	27.8	13	1	MTCMAD melanotropin alpha
4	25	27.8	13	1	MTHOAD melanotropin alpha
5	24	26.7	15	2	JN0730 hypothetical 1.7K
6	23	25.6	11	2	A34243 H-hyosphorin - Ja
7	23	25.6	15	2	PH0760 T-cell receptor be
8	22	24.4	8	2	A31570 angiotensin-conver
9	21	23.3	11	2	YHRT morphogenetic neur
10	21	23.3	11	2	YHNU morphogenetic neur
11	21	23.3	11	2	YHBO morphogenetic neur
12	21	23.3	11	2	YHXA morphogenetic neur
13	21	23.3	11	2	YHFX morphogenetic neur
14	21	23.3	12	2	S6730 hemoglobin, extrac
15	21	23.3	12	2	146922 gene Bata protein
16	21	23.3	13	2	A3734 encephalin precurs
17	21	23.3	13	2	150173 alpha-2 collagen -
18	21	23.3	13	2	S01904 H+-transporting AT
19	21	23.3	13	2	A86126 hypothetical prote
20	21	23.3	14	2	S2376 collagen alpha cha
21	21	23.3	16	2	PH0748 T-cell receptor be
22	20	22.2	10	2	B33710 ornithine decarbox
23	20	22.2	10	2	A55695 proteoglycan core
24	20	22.2	12	2	S65629 protoporphyrinogen
25	20	22.2	13	2	S04013 lignin peroxidase
26	20	22.2	13	2	PH0928 T-cell receptor be
27	20	22.2	14	2	S13864 methyl coenzyme M
28	20	22.2	14	2	A59018 MUC1 enhancer bind
29	20	22.2	15	2	T46625 hypothetical prote

30	20	22.2	15	2	D28587	T-cell receptor be
31	20	22.2	16	1	MTRFBS	melanotropin beta
32	20	22.2	16	2	G45681	orf 61.1 - phage T
33	20	22.2	16	2	S36876	aquacobalamin redu
34	19	21.1	11	2	A34662	actinina cardio-ex
35	19	21.1	11	2	D56979	collagen alpha 1(I
36	19	21.1	13	2	T08533	hypothetical prote
37	19	21.1	13	2	S22995	hypothetical prote
38	19	21.1	13	2	S13273	polyisobutylglyc
39	19	21.1	13	2	S57567	T cell receptor V-
40	19	21.1	13	2	G83988	hypothetical prote
41	19	21.1	15	2	S21241	oligo-1,6-glucosid
42	19	21.1	15	2	PA0102	fructose-bisphosph
43	19	21.1	16	2	B28587	T-cell receptor be
44	19	21.1	16	2	F53284	T-cell receptor be
45	19	21.1	16	2	PH0767	T-cell receptor be

ALIGNMENTS

RESULT 1
154945
gene C protein - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 08-Oct-1999
C:Accession: 154945
R:Tao, T.; Bourne, J.C.; Blumenthal, R.M.
J. Bacteriol. 173, 1367-1375, 1991
A:Title: A family of regulatory genes associated with type II restriction-modificatio
A:Reference number: 154945; MUID:91139577
A:Accession: 154945
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14 <RBS>
A:Cross-references: GB:M63619; NID:q147664; PIDN:AAA24555.1; PID:q147665

Query Match Score 26; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 6.7e+02; Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 RNVLLEKK 12
DB 2 KEVIMLEKK 9

RESULT 2

ES8501
25K kidney and gallbladder stone protein - unidentified bacterium (fragment)

C:Species: unidentified bacterium

C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C:Accession: ES8501

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A:Description: The proteins of kidney and gallbladder stones.

A:Reference number: AS8501

A:Accession: ES8501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BIN>

A:Experimental source: human kidney and gallbladder stones

A:Note: tentative identification of 8-Gly and 13-Ser

Query Match Score 26; DB 2; Length 16;

Best Local Similarity 60.0%; Pred. No. 7.6e+02; Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 KGNVLEKK 12
DB 6 KGNVLSKE 15

RESULT 3

MTCMAD
melanotropin alpha - Arabian camel
C:Species: Camelus dromedarius (Arabian camel)
C:Date: 13-Jul-1991 #sequence_revision 13-Jul-1991 #text_change 20-Mar-1998
C:Accession: A01464
R:Li, C.H.; Danho, W.O.; Chung, D.; Rao, A.J.
Biochemistry 14, 947-952, 1975
A:Title: Isolation, characterization, and amino acid sequence of melanotropins from camel
A:Reference number: A90393; MUID:75146434
A:Accession: A01464
A:Molecule type: protein
A:Residues: 1-13 <LIC>
C:Superfamily: corticotrophin-11potropin
F:1/Modified site: acetylated amino end; blocked carboxyl end; hormone; pituitary
F:1/Modified site: acetylated amino end (Ser) (partial) #status experimental
F:13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KWGAP 16
DB 8 RWGKP 12

RESULT 4
MTHOAD
melanotropin alpha - horse
C:Species: Equus caballus (domestic horse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 20-Mar-1998
C:Accession: A91785; A01464
R:Dixon, J.S.; Li, C.H.
J. Am. Chem. Soc. 82, 4568-4572, 1960
A:Title: The isolation and structure of alpha-melanocyte-stimulating hormone from horse
A:Reference number: A91785
A:Accession: A91785
A:Molecule type: protein
A:Residues: 1-13 <DIX>
C:Superfamily: corticotrophin-11potropin
F:1/Modified site: blocked amino end (Ser) (probably acetylated) #status experimental
F:13/Modified site: blocked carboxyl end (Val) (probably amidated) #status experimental

Query Match 27.8%; Score 25; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 9.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 KWGAP 16
DB 8 RWGKP 12

RESULT 5
JN0730
hypotheical 1.7k protein - phage SPPI
N:Alternate names: hypothetical protein 42.1
C:Species: phage SPPI
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 17-Mar-1999
C:Accession: JN0730
R:Chai, S.; Szepan, U.; Lueder, G.; Trautner, T.A.; Alonso, J.C.
Gene 129, 41-49, 1993
A:Title: Sequence analysis of the left end of the Bacillus subtilis bacteriophage SPPI
A:Reference number: JN0729; MUID:93328123
A:Accession: JN0730
A:Molecule type: DNA
A:Residues: 1-15 <CHA>
A:Cross-references: EMBL:X65941

Query Match 26.7%; Score 24; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPKGRNVLE 9
DB 5 GPPFRSMVL 13

RESULT 6
A34243
H-hyosophorin - Japanese flounder (fragment)
C:Species: Paralichthys olivaceus (Japanese flounder)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 12-Feb-1999
C:Accession: A34243
R:Seiko, A.; Kitajima, K.; Iwasaki, M.; Inoue, S.; Inoue, Y.
J. Biol. Chem. 264, 15922-15929, 1989
A:Title: Structural studies of fertilization-associated carbohydrate-rich glycoprotein
of a novel penta-antennary N-linked glycan chain in the tandem repeating glycopeptide
A:Reference number: A34243; MUID:89380184
A:Accession: A34243
A:Molecule type: protein
A:Residues: 1-11 <SEK>
A>Note: 3-Ala, 4-Ala, 5-Pro or Gln, and 6-Val were also found

Query Match 25.6%; Score 23; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPKGRNVLE 10
DB 2 GSVGGNVTLTD 11

RESULT 7
PH0760
T-cell receptor beta chain (H2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0760
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846
A:Accession: PH0760
A:Molecule type: mRNA
A:Residues: 1-15 <CAS>
A:Cross-references: EMBL:X60855; NID:g51194; PIDN:CAA43245.1; PID:g51195
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 25.6%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PKGRN 6
DB 5 PTGRN 9

RESULT 8
A31570
angiotensin-converting enzyme inhibitor - yellowfin tuna
C:Species: Thunnus albacares (yellowfin tuna)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Aug-2000
C:Accession: A31570
R:Kohama, Y.; Matsumoto, S.; Oka, H.; Teramoto, T.; Okabe, M.; Mimura, T.
Biochem. Biophys. Res. Commun. 155, 332-337, 1988
A:Title: Isolation of angiotensin-converting enzyme inhibitor from tuna muscle.
A:Accession: A31570; MUID:88326322
A:Molecule type: protein
A:Residues: 1-8 <KOH>
A>Note: the source is designated as Neothunnus macropterus
C:Superfamily: unassigned animal peptides
C:Keywords: angiotensin-converting enzyme inhibitor

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:12 : Search time 6.5 Seconds
(without alignments)
95.310 Million cell updates/sec

Title: US-09-847-637B-2
Perfect score: 90
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 814

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SWISSPROT_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.5	28.3	15	LCK_DROME	P81829 drosophila
2	25	27.8	13	MLA_ANOCA	P41589 anolis caro
3	25	27.8	13	MLA_CAMDR	P01198 camelus albi
4	22	24.4	8	ACT_THUDL	P18691 thunnus albu
5	21	23.3	11	MORN_HUMAN	P01163 homo sapien
6	20	22.2	13	LIGA_TYRAVE	P20011 tirametes ve
7	20	22.2	16	MLB_SQUAC	P01207 squatus aca
8	19	21.1	9	TKL1_LOCMT	P16223 locusta mig
9	19	21.1	11	CEP1_ACHFU	P22790 achalina fu
10	19	21.1	12	UP01_CAEEL	P55954 caenorhabd
11	19	21.1	13	IDHP_RAT	P56574 rattus norv
12	19	21.1	15	UC06_MAIZE	P80612 zea mays (m
13	19	21.1	16	MMPX_SOLTU	P80501 solanum tub
14	18	20.0	9	CONO_CONGE	P05486 conus geogr
15	18	20.0	10	BPP8_BOTIN	P30426 bothrops in
16	18	20.0	10	BPP_VIPAS	P13151 vipera aspi
17	18	20.0	12	PSR3_PHYPA	P80662 physcomite
18	18	20.0	13	CAAL_CONST	P13471 conus stria
19	18	20.0	13	PSBP_PINPS	P81668 pinus pinas
20	18	20.0	14	TAT_HV1W2	P12511 human immun
21	18	20.0	14	TAT_HV1Z8	P80072 bacillus th
22	18	20.0	15	MALT_BACTO	P30425 bothrops in
23	17.5	19.4	5	BPP7_BOTIN	P13137 mytilus edu
24	17	18.9	6	CIF2_MYTEO	P41491 locusta mig
25	17	18.9	6	LOK1_LOCMT	P21141 leucophaea
26	17	18.9	8	LCK1_LEUMA	P21141 leucophaea
27	17	18.9	8	LCK2_LEUMA	P21141 leucophaea
28	17	18.9	8	LCK3_LEUMA	P21141 leucophaea
29	17	18.9	8	LCK4_LEUMA	P21141 leucophaea
30	17	18.9	8	LCK5_LEUMA	P19987 leucophaea
31	17	18.9	8	LCK6_LEUMA	P19987 leucophaea
32	17	18.9	8	LCK7_LEUMA	P19989 leucophaea
33	17	18.9	8	LCK8_LEUMA	P19990 leucophaea

34	17	18.9	9	SAP_STOVA	P24047 stomopneute
35	17	18.9	10	FAR6_PANRE	P82660 panagrellus
36	17	18.9	10	HTF1_ROMMI	P18110 romanes mlt
37	17	18.9	10	HTF2_CARMO	P11385 carausius m
38	17	18.9	10	HTF_HELZE	P16353 heliothis z
39	17	18.9	10	HTF_NAUCI	P10939 nauphoeta c
40	17	18.9	10	HTF_TABAT	P14596 tabanus acr
41	17	18.9	10	LABA_JATMU	P13370 jatropa mu
42	17	18.9	10	TPIS_NICPL	P19118 nicotiana p
43	17	18.9	13	LMA1_LOCMT	P38496 locusta mig
44	17	18.9	14	SAP2_ARBPU	P11760 arbutus pun
45	17	18.9	15	ACT_PINPS	P81085 pinus pinas

ALIGNMENTS

RESULT 1	LCK_DROME	STANDARD:	PRT:	15 AA.
ID	LCK_DROME			
AC	P81829:	30-MAY-2000 (rel. 39, Created)		
DT	30-MAY-2000 (rel. 39, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Leucokinin (DLK).			
GN	pp or DLK.			
OS	Drosophila melanogaster (Fruit fly).			
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;			
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;			
OC	Ephydroidea; Drosophilidae; Drosophila.			
OX	NCBI_TaxID=7227;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Neurosecretory cell;			
RC	MEDLINE=20044845; PubMed=1057474;			
RA	Ternhez S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,			
RA	Veenstra J.A., Dow J.A.T.;			
RT	*Isolation and characterization of a leucokinin-like peptide of			
RT	Drosophila melanogaster.;			
RT	J. Exp. Biol. 202:3667-3676(1999).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BERKELEY;			
RA	Celniker S.E., Aghayani A., Arcaina T.T., Baxter E., Blazek R.G.,			
RA	Butenkov C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,			
RA	Fairlan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,			
RA	Houston K.A., Hummasti S.R., Kaira K., Kearney L., Kim E., Lee B.,			
RA	Lewis S., Li P., Lomtan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,			
RA	Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Segreia A.,			
RA	Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,			
RA	Zietan U.L., Rubin G.M.;			
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.			
CC	- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE			
CC	STELATE CELLS TO RAISE CHLORIDE CONDUCTANCE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation-			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL: AC006496; - NOT_ANNOTATED_CDS.			
DR	FLYbase: Fggn0028418; Leucokinin.			
KW	Neuropeptide; Amidation.			
FT	MOD_RES 15 15			
SO	SEQUENCE 15 AA; 1743 MM; 4793A08F251C9525 CRC64;			
Query Match	28.3%;	Score 25.5;	DB 1;	Length 15;
Best local Similarity	50.0%;	Pred. No. 4e+02;		
Matches	7;	Conservative	1;	Mismatches 1;

OY 6 NVLEK-----WG 14
 :|||
 DB 2 SVLGGKORFHSWG 15

RESULT 2

MIA_ANOCA STANDARD: PRT: 13 AA.
 ID MIA_ANOCA
 AC P41589;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin alpha (Alpha-MSH).
 OS Anolis carolinensis (Green anole) (American chameleon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotinae; Anolis.
 OX NCBI_TaxID=28377;
 RN [1]
 RP SEQUENCE.
 RT TISSUE=Pituitary;
 MEDLINE=92270473; PubMed=1667689;
 RA Dorez R.M., Lancha A., Rand-Weaver M., Jankelow L., Adamczyk D.L.;
 RT "Detection of a novel sequence change in the major form of alpha-MSH
 RT isolated from the intermediate pituitary of the reptile, Anolis
 RT carolinensis."
 RL Peptides 12:1261-1266(1991).
 CC -1 SIMILARITY: BELONGS TO THE POMC FAMILY.
 KW Hormone; Amidation.
 FT MOD.RES 13
 SQ SEQUENCE 13 AA; 1608 MW; FF990A7358B09C1 CRC64;

Query Match 27.8%; Score 25; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4.2e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KWGAP 16
 :|||
 DB 8 RWGKP 12

RESULT 3

MIA_CAMDR STANDARD: PRT: 13 AA.
 ID MIA_CAMDR
 AC P01198;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Melanotropin alpha (Alpha-MSH).
 OC Camelus dromedarius (Dromedary) (Arabian camel), and
 OC Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 OX NCBI_TaxID=9838, 9796;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.dromedarius;
 RA MEDLINE=75146434; PubMed=1125179;
 RA Li C.H., Danho W.O., Chung D., Rao A.J.;
 RT "Isolation, characterization, and amino acid sequence of
 RT melanotropins from camel pituitary glands."
 RL Biochemistry 14:947-952(1975).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=Horse; TISSUE=Pituitary;
 RA Dixon J.S., Li C.H.;
 RT "The isolation and structure of alpha-melanocyte-stimulating hormone
 RT from horse pituitaries."
 RL J. Am. Chem. Soc. 82:4568-4572(1960).
 CC -1 SIMILARITY: BELONGS TO THE POMC FAMILY.
 DR PIR: A01464; MTCMAD.
 DR PIR: A91785; MTHOAD.
 KW Hormone; Acetylation; Amidation.
 FT MOD.RES 1
 ACETYLATION (IN ABOUT 508 OF CAMEL

FT MOD.RES 13 13 MOLECULES).
 SQ SEQUENCE 13 AA; 1624 MW; FF991CA958B09C1 CRC64;
 Amidation.

Query Match 27.8%; Score 25; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 4.2e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 12 KWGAP 16
 :|||
 DB 8 RWGKP 12

RESULT 4

ACT_THUAL STANDARD: PRT: 8 AA.
 ID ACT_THUAL
 AC P18691;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Angiotensin-converting enzyme inhibitor.
 OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Scombroidei;
 OC Scombridae; Thunnus.
 OX NCBI_TaxID=8236;
 RN [1]
 RP SEQUENCE.
 RT TISSUE=Muscle;
 MEDLINE=88326322; PubMed=3415688;
 RA Kohama Y., Matsunoto S., Oka H., Teramoto T., Okabe M., Mimura T.;
 RT "Isolation of angiotensin-converting enzyme inhibitor from tuna
 RT muscle."
 RL Biochem. Biophys. Res. Commun. 155:332-337(1988).
 DR PIR: A31570; A31570.
 SQ SEQUENCE 8 AA; 953 MW; 6AA863733051F1B7 CRC64;

Query Match 24.4%; Score 22; DB 1; Length 8;
 Best Local Similarity 100.0%; Pred. No. 1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 KWG 14
 :|||
 DB 5 KWG 7

RESULT 5

MORN_HUMAN STANDARD: PRT: 11 AA.
 ID MORN_HUMAN
 AC P01163;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Morphogenetic neuropeptide (Head activator) (HA).
 OS Homo sapiens (Human).
 OS Rattus norvegicus (Rat).
 OS Bos taurus (Bovine).
 OS Anthopleura elegantissima (Sea anemone), and
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606, 10116, 9913, 6110, 6087;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=Human, Rat, and Bovine;
 MEDLINE=82035850; PubMed=7290191;
 RA Bodenmuller H., Schaller H.C.;
 RT "Conserved amino acid sequence of a neuropeptide, the head activator,
 RT from coelenterates to humans."
 RL Nature 293:579-580(1981).
 RN [2]
 RP SEQUENCE.

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:33 : Search time 20 Seconds
(without alignments)
136.396 Million cell updates/sec

Title: US-09-847-637b-2
Perfect score: 90
Sequence: 1 GPKGRNVLEKKMGAP 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

1 number of hits satisfying chosen parameters: 3277

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protist:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	26	28.9	14	2	Q47599		Q47599 escherichia
2	25	27.8	10	11	070580		070580 mus musculus
3	25	27.8	15	9	Q38427		Q38427 bacterioph
4	24	26.7	10	4	Q9UNF2		Q9UNF2 homo sapien
5	24	26.7	11	4	Q60842		Q60842 homo sapien
6	24	26.7	15	2	Q9R4P5		Q9R4P5 brevidimion
7	23	25.6	11	15	Q83410		Q83410 mouse mamma
8	23	25.6	13	15	Q85645		Q85645 mouse mamma
9	23	25.6	16	4	Q9UCI8		Q9UCI8 homo sapien
10	23	25.6	16	8	Q9T2V8		Q9T2V8 homo sapien
11	23	25.6	16	10	Q9SBD6		Q9SBD6 triticum ae
12	22	24.4	14	2	Q9R517		Q9R517 escherichia
13	22	24.4	14	10	P82322		P82322 pisum sativ
14	21.5	23.9	13	5	Q9W506		Q9W506 diosophila
15	21	23.3	8	8	Q94VB5		Q94VB5 varanus sal
16	21	23.3	8	8	Q94VB2		Q94VB2 varanus sal

17	21	23.3	8	8	Q94VA7	Q94VA7 varanus sal
18	21	23.3	8	8	Q94PX7	Q94PX7 felis libyc
19	21	23.3	8	8	Q94PX6	Q94PX6 felis libyc
20	21	23.3	8	8	Q94PX5	Q94PX5 felis libyc
21	21	23.3	9	8	Q94VC6	Q94VC6 varanus pil
22	21	23.3	10	8	Q94VD5	Q94VD5 varanus pil
23	21	23.3	12	7	Q31006	Q31006 bos taurus
24	21	23.3	13	7	Q9TNO8	Q9TNO8 homo sapien
25	21	23.3	13	8	Q9MOK6	Q9MOK6 rupicapra r
26	21	23.3	13	8	Q9MOK3	Q9MOK3 capra ibex
27	21	23.3	13	8	Q9MOK0	Q9MOK0 cervus elap
28	21	23.3	15	4	Q00604	Q00604 homo sapien
29	21	23.3	15	4	Q9BXX4	Q9BXX4 homo sapien
30	21	23.3	15	8	P92076	P92076 euhadra her
31	21	23.3	16	5	Q9TWS8	Q9TWS8 lamellibrac
32	21	23.3	16	5	Q9NFJ0	Q9NFJ0 trypanosoma
33	20	22.2	8	4	Q16468	Q16468 homo sapien
34	20	22.2	10	2	Q9R7J8	Q9R7J8 helicobacte
35	20	22.2	10	11	Q63389	Q63389 rattus norv
36	20	22.2	11	2	Q9EUZ3	Q9EUZ3 escherichia
37	20	22.2	12	4	Q9UMQ9	Q9UMQ9 homo sapien
38	20	22.2	12	4	Q9H4X3	Q9H4X3 homo sapien
39	20	22.2	13	1	Q50831	Q50831 mechanococc
40	20	22.2	15	10	Q9S8V7	Q9S8V7 triticum ae
41	20	22.2	16	2	Q45530	Q45530 bacillus su
42	20	22.2	16	5	Q9PMK0	Q9PMK0 mytilus edu
43	20	22.2	16	5	Q9TWK1	Q9TWK1 mytilus edu
44	19.5	21.7	14	10	Q941T6	Q941T6 fragaria nu
45	19	21.1	8	8	Q94VB2	Q94VB2 varanus yuw

ALIGNMENTS

RESULT 1	
ID Q47599	PRELIMINARY: PRT: 14 AA.
AC Q47599:	
DT 01-NOV-1996 (TREMBlrel. 01, Created)	
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)	
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)	
DE C (FRAGMENT).	
GN	
OS Escherichia coli.	
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC Escherichia.	
OX NCBI_TaxID=562;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=91139577; PubMed=1995588;	
RA Tao T., Bourne J.C., Blumenthal R.M.;	
RT "A family of regulatory genes associated with type II restriction-	
RT modification systems.";	
RL J. Bacteriol. 173:1367-1375(1991).	
DR EMBL: M63619; AAA2455.1; -.	
FT NON_TER	
SQ SEQUENCE 14 AA: 1705 MM: 77B6CA60581A4F3B CRC64:	
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Best Local Similarity	50.0%; Pred. NO. 9.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;	
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AC Q70580:	
DT 01-AUG-1998 (TREMBlrel. 07, Created)	
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)	

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DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE III (FRAGMENT).
GN CAR3 OR CAR3 OR CA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene.";
RL Gene 214:157-165(1999).
DR EMBL; AJ006474; CAA07057.1; -.
DR MGD; MGI:1351477; Cars.
DR MGD; MGI:88270; Cars3.
FT NON_TER
FT 10
SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;

Query Match 27.8%; Score 25; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 9.6e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 9 LEKKMGAP 16
DB 1 MAKEWATP 8

RESULT 3
O38427 PRELIMINARY; PRT; 15 AA.
ID O38427;
AC O38427;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CORE PROTEIN (FRAGMENT).
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like phages.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=65083058; PubMed=6512858;
RA Keller B., Sengstag C., Kellenberger E., Bickie T.A.;
RT "Gene 68, a new bacteriophage T4 gene which codes for the 17K prohead
core protein is involved in head size determination.";
RL J. Mol. Biol. 179:415-430(1984).
FT NON_TER
FT 15
SQ SEQUENCE 15 AA; 1713 MW; 1B455B28262C0229 CRC64;

Query Match 27.8%; Score 25; DB 9; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 8 VLEKKMGAP 16
DB 6 LIETWCKP 14

RESULT 4
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ID O90NF2;
AC O90NF2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE ALPHA 1 COLLAGEN (FRAGMENT).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BREAST;
RA Ratcliffe T.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
at 10,828 bp: cytosine replaces adenine.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF128441; AAD32608.1; -.
RN Collagen.
FT NON_TER
FT 1
FT NON_TER
FT 10
SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 26.7%; Score 24; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GPKG 4
DB 4 GPKG 7

RESULT 5
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ID O60842;
AC O60842;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE (FRAGMENT).
GN CA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene.";
RL Gene 214:157-165(1999).
DR EMBL; AJ006473; CAA07056.1; -.
FT NON_TER
FT 11
SQ SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 26.7%; Score 24; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 9 LEKKMG 14
DB 1 MAKEMG 6

RESULT 6
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ID O9R4P5;
AC O9R4P5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE RIBOSOMAL PROTEIN L24 (FRAGMENT).
OS Brevudinonas diminuta (Pseudomonas diminuta).
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Brevudinonas.
OX NCBI_TaxID=293;
RN [1]
RP SEQUENCE.
RA MEDLINE=95244309; PubMed=7727274;
RX Ochi K.;
RT "Comparative ribosomal protein sequence analyses of a phylogenetically
defined genus, Pseudomonas, and its relatives.";
RL Int. J. Syst. Bacteriol. 45:268-273(1995).
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:42:03 : Search time 10.5 Seconds
(without alignments)
37.220 Million cell updates/sec

Title: US-09-847-637B-2

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Sequence: 1 GPKGRNVLEKKWGAP 16

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Gapop 10.0, Gapext 0.5

Searched: 231628 segs, 24425594 residues

al number of hits satisfying chosen parameters: 106182

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	40.0	8	2	US-08-467-822-11
2	36	40.0	8	4	US-08-432-697-11
3	36	40.0	8	4	US-08-466-248-11
4	30	33.3	14	4	US-08-584-043A-80
5	30	33.3	16	4	US-08-602-999A-228
6	29	32.2	13	5	PCT-US95-07543-3
7	28	31.1	16	1	US-08-300-386A-38
8	28	31.1	16	3	US-08-931-645-38
9	28	31.1	16	5	PCT-US94-01258-38
10	28	31.1	16	5	PCT-US95-11235-38
11	27	30.0	9	1	US-08-452-083-23
12	27	30.0	9	1	US-08-468-557-12
13	27	30.0	10	2	US-08-556-597-158
14	27	30.0	15	3	US-08-491-954-9
15	26	28.9	6	1	US-08-076-092-56
16	26	28.9	6	2	US-08-730-486-56
17	26	28.9	7	1	US-08-076-092-53
18	26	28.9	7	1	US-08-730-486-53
19	26	28.9	8	1	US-08-076-092-49
20	26	28.9	8	2	US-08-621-803-237
21	26	28.9	8	2	US-08-621-803-237
22	26	28.9	8	2	US-08-621-259A-239
23	26	28.9	8	2	US-08-621-259A-243
24	26	28.9	8	2	US-08-730-486-49
25	26	28.9	8	4	US-09-296-284-14
26	26	28.9	8	4	US-09-217-352-237
27	26	28.9	9	1	US-08-076-092-42

28	26	28.9	9	2	US-08-730-486-42	Sequence 42, App1
29	26	28.9	9	3	US-09-188-579-109	Sequence 109, App
30	26	28.9	9	4	US-09-315-444-109	Sequence 109, App
31	26	28.9	10	3	US-08-159-339A-812	Sequence 812, App
32	26	28.9	11	6	5248606-34	Patent No. 5248606
33	26	28.9	12	1	US-07-778-233B-36	Sequence 36, App1
34	26	28.9	12	1	US-07-963-321-36	Sequence 36, App1
35	26	28.9	12	1	US-08-290-641-36	Sequence 36, App1
36	26	28.9	12	1	US-08-330-599-10	Sequence 10, App1
37	26	28.9	12	1	US-08-548-540-36	Sequence 36, App1
38	26	28.9	12	2	US-08-726-306A-156	Sequence 156, App1
39	26	28.9	12	5	PCT-US96-09809-36	Sequence 36, App1
40	26	28.9	13	1	US-08-462-894-27	Sequence 27, App1
41	26	28.9	13	1	US-08-206-185-27	Sequence 27, App1
42	26	28.9	13	1	US-07-907-190-8	Sequence 8, App1
43	26	28.9	15	1	US-08-111-939-10	Sequence 10, App1
44	26	28.9	16	2	US-08-637-759B-428	Sequence 428, App
45	26	28.9	16	3	US-08-871-355A-428	Sequence 428, App

ALIGNMENTS

RESULT 1
US-08-467-822-11
; Sequence 11, Application US/08467822
; Patent No. 5843460
; GENERAL INFORMATION:
; APPLICANT: Labigne, Agnes
; APPLICANT: Sauerbaum, Sebastien
; APPLICANT: Ferrero, Richard L.
; APPLICANT: Thibierge, Jean-Michel
; TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
; TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
; TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,822
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,177
; FILING DATE: 19-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/432,697
; FILING DATE: 02-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION/DOCKET NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03495.0137-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-467-822-11

Query Match 40.0%; Score 36; DB 2; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GPKGRNV 8

RESULT 2
US-08-432-697-11
Sequence 11, Application US/08432697
Patent No. 6248330

GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0137-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-432-697-11

Query Match 40.0%; Score 36; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GPKGRNV 8

RESULT 3
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Sequence 11, Application US/08466248

Patent No. 6258359
GENERAL INFORMATION:

APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495, 0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-248-11

Query Match 40.0%; Score 36; DB 4; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.7e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 2 GPKGRNV 8

RESULT 4
US-08-584-043A-80
Sequence 80, Application US/08584043A
Patent No. 6344436

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauer, Jochen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
TITLE OF INVENTION: MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 17, 2002, 17:38:52 ; Search time 25 Seconds
(without alignments)
71.087 Million cell updates/sec

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Post-processing: Minimum Match 0%
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SUMMARIES

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6	55	63.2	16	21	AAV93329
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9	39	44.8	16	18	AAW43460
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11	35	40.2	16	17	AAW10516

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13	31	35.6	12	22	AAW0858
14	31	35.6	15	12	AAW14808
15	31	35.6	15	20	AAV34136
16	31	35.6	15	21	AAV52607
17	31	35.6	15	21	AAV52656
18	30	34.5	10	21	AAW32456
19	30	34.5	10	21	AAW54380
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22	30	34.5	14	18	AAW24451
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26	28	32.2	9	19	AAW56753
27	28	32.2	12	18	AAW38002
28	28	32.2	15	22	AAW00664
29	28	32.2	15	19	AAW37382
30	27	31.0	7	22	AAW44111
31	27	31.0	7	22	AAW6151
32	27	31.0	7	22	AAW6450
33	27	31.0	9	19	AAW5452
34	27	31.0	10	18	AAW32769
35	27	31.0	10	22	AAW87932
36	27	31.0	10	22	AAW87933
37	27	31.0	10	22	AAW87935
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41	27	31.0	13	18	AAW01659
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44	27	31.0	14	19	AAW64583
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ALIGNMENTS

RESULT 1
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ID AAV93330 standard; peptide; 16 AA.
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AC AAV93330:
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DT 04-SEP-2000 (first entry)
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DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
XX
KW Inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN WO200027870-A1.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99WO-IL00595.
XX
PR 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
XX
PI Naparstek Y, Ulmansky R, Kasht Y;
XX
DR WPI: 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
XX
PT immunity against autoimmune disease or inflammatory disorders,
XX
PS especially arthritis -
XX
PS Claim 3; Page 7; 58pp; English.

Peptide from libra
Melanocyte stimula
fes oncogene prote
variant human pota
v-fes encoded onco
tps-encoded oncopr
Human secreted pro
Amino acid sequenc
Human scavenger re
Delivery peptide u
Nucleic acid (NA)
N terminal of haem
Grb2 N-terminal SH
Human tumor-associ
A. tumefaciens ant
WR domain binding
Human protein frag
Hepatitis C virus
H11 binding site c
H11 binding site c
H11 binding site c
Mycobacterial isol
Human platelet gly
Saccharomyces cere
Saccharomyces cere
Oregon green 514 b
Oregon green 514 b
Reactive peptide v
Coleopteran antiba
Peptide MS-36, wit
Peptide MS-37, wit
Human Factor V pro
Peptide fragment o

xx The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of *Mycobacterium tuberculosis*. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 CC

SO Sequence 16 AA:

Query Match 100.0%; Score 87; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e-08;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTNDG 16
 Db 1 VLEKKMGAPTTNDG 16

AAW43458 standard; peptide: 16 AA.

AAW43458;

08-APR-1998 (first entry)

Mycobacteria sp. hsp68 derived peptide (group 1 #8).

Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 rheumatoid arthritis; antigen; infectious disease; prophylactic;
 pristane induced arthritis; PIA.

Synthetic.
Mycobacteria sp.

W09711966-A1.

03-APR-1997.

26-SEP-1996; 96WO-GB02382.

27-SEP-1995; 95GB-0019737.

(PEPT-) PEPTIDE THERAPEUTIC LTD.

Elson CJ, Thompson JS;

WPI: 1997-212851/19.

Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis

Disclosure: Fig 1a; 91pp; English.

This peptide is one of a library (see AAW43451-W43556) which represents
 the mycobacterial heat shock protein, hsp65 and is designed to study
 a novel method for the treatment of autoimmune disease e.g. rheumatoid
 arthritis. This fragment has been allocated as a group 1 peptide which
 is composed of the fragments found in AAW43451 to AAW43460. Mycobacterial
 hsp65 is known to be an immunodominant antigen in a number of infectious
 diseases and is linked to pristane induced arthritis (PIA) in vitro,
 however heat shock proteins and peptides derived from microbial sources
 may act as self antigens and thus have limited clinical use. The human
 hsp65 homologue, hsp58, or fragments of the hsp58 protein
 (see AAW43498-W4350) may be useful in the development of vaccines for
 prophylaxis or treatment of an autoimmune disease such as rheumatoid
 arthritis.

Sequence 16 AA:

Query Match 93.1%; Score 81; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTND 15
 Db 2 VLEKKMGAPTTND 16

AAW4780 standard; peptide: 16 AA.

AAW4780;

11-NOV-1996 (first entry)

Peptide from library spanning whole of hsp65.

Hsp: heat shock protein; *Mycobacterium bovis*; microbial; diagnosis;
 rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 prophylaxis.

Synthetic.

W09610039-A1.

04-APR-1996.

27-SEP-1995; 95WO-GB02295.

27-SEP-1994; 94GB-0019553.

(PEPT-) PEPTIDE THERAPEUTICS LTD.

Elson CJ, Thompson SJ;

WPI: 1996-20088/20.

Polypeptide derived from bacterial heat shock protein 65 - for use
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 rheumatoid arthritis.

Example 1; Figure 1; 88pp; English.

AAW4773-R94878 are overlapping peptides of a library spanning the
 whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 prepared from the library and used to immunise mice, after 10 days the
 mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 peptide was found to correspond to residues 21-31 of full length hsp65
 (see AAW4772). Peptides contg. this sequence are used in the diagnosis,
 treatment and prophylaxis (may be used in a vaccine) of autoimmune
 diseases such as rheumatoid arthritis.

Sequence 16 AA:

Query Match 87.4%; Score 76; DB 17; Length 16;

Best Local Similarity 93.3%; Pred. No. 2.2e-06;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLEKKMGAPTTND 15
 Db 2 VLEKKMGAPTTND 16

AAW43459 standard; peptide: 15 AA.

AAW43459;

08-APR-1998 (first entry)

Query Match 93.1%; Score 81; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KM pristanol induced arthritis; PIA.
 XX
 OS Synthetic.
 OS Mycobacteria sp.
 XX
 PN WO9711966-A1.
 XX
 XX 03-APR-1997.
 PD
 XX 26-SEP-1996; 96WO-GB02382.
 PF
 XX 27-SEP-1995; 95GB-0019737.
 PR
 XX (PEPT-) PEPTIDE THERAPEUTIC LTD.
 PA
 XX Elson CJ, Thompson JS;
 PI
 WPI: 1997-212851/19.
 PT Polypeptide(s) derived from microbial heat shock protein - useful
 PT for treatment of autoimmune disease esp. arthritis
 XX
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAM43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristanol induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAM43451-W43556) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 CC
 XX
 SQ Sequence 15 AA:
 Query Match 80.5%; Score 70; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.2e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 5 KKWGAPTTNDG 16
 1 KKWGAPTTNDG 12

XX
 PR 27-SEP-1994; 94GB-0019553.
 XX
 XX (PEPT-) PEPTIDE THERAPEUTICS LTD.
 PA
 XX
 PI Elson CJ, Thompson SJ;
 XX
 DR WPI: 1996-200888/20.
 XX
 XX Polypeptide derived from bacterial heat shock protein 65 - for use
 PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 PT rheumatoid arthritis.
 XX
 PS Example 1; Figure 1; 88pp; English.
 XX
 CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristanol to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.
 CC
 XX
 SQ Sequence 15 AA:
 Query Match 74.7%; Score 65; DB 17; Length 15;
 Best Local Similarity 91.7%; Pred. No. 0.00016;
 Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 5 KKWGAPTTNDG 16
 1 KKWGAPTTNDG 12

RESULT 6
 AAY93329
 ID AAY93329 standard; peptide; 16 AA.
 XX
 AC AAY93329;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Amino acid sequence of an epitope of heat shock protein 60.
 XX
 KW Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;
 KW inflammatory disorder; arthritis.
 XX
 OS Mycobacterium tuberculosis.
 OS
 PN WO200027870-A1.
 PN
 XX 18-MAY-2000.
 PD
 XX 04-NOV-1999; 99WO-IL00595.
 PF
 XX 05-NOV-1998; 98US-0107213.
 PR
 XX (HADA-) HADASIT MEDICAL RES SERVICES & DEV.
 PA
 XX Naparstek Y, Ulmansky R, Kashi Y;
 PI
 XX WPI: 2000-376486/32.
 DR
 XX Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -
 XX
 PS Claim 2; Page 7; 58pp; English.
 PS
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the

CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.
 CC

SO Sequence 16 AA;

Query Match 63.2%; Score 55; DB 21; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.0094;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 10
 |||||
 DB 7 VLEKKMGAP 16

RESULT 7
 AAR94779
 ID AAR94779 standard; peptide: 15 AA.

AAR94779;

DT 11-NOV-1996 (first entry)

XX Peptide from library spanning whole of hsp65.

DE Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
 KW rheumatoid arthritis; autoimmune disease; treatment; vaccine;
 KW prophylaxis.

OS Synthetic.

PN W09610039-A1.

PD 04-APR-1996.

PF 27-SEP-1995; 95WO-GB02295.

PR 27-SEP-1994; 94GB-0019553.

PA (PEPT-) PEPTIDE THERAPEUTICS LTD.

PI Elson CJ, Thompson SJ;

DR WPI: 1996-200888/20.

PT Polypeptide derived from bacterial heat shock protein 65 - for use
 in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
 rheumatoid arthritis.

PS Example 1; Figure 1; 88pp; English.

CC AAR94773-R94878 are overlapping peptides of a library spanning the
 CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
 CC prepared from the library and used to immunise mice, after 10 days the
 CC mice received injections of pristane to induce arthritis and the
 CC animals examined for incidence of arthritis. A preferred anti-arthritis
 CC peptide was found to correspond to residues 21-31 of full length hsp65
 CC (see AAR94772). Peptides contg. this sequence are used in the diagnosis,
 CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
 CC diseases such as rheumatoid arthritis.

SO Sequence 15 AA;

Query Match 55.2%; Score 48; DB 17; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 9
 |||||
 DB 7 VLEKKMGAP 15

RESULT 8
 AAM43457
 ID AAM43457 standard; peptide: 15 AA.

XX AAM43457;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #7).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;
 KW pristane induced arthritis; PIA.

OS Synthetic.

PN W09711966-A1.

PD 03-APR-1997.

PF 26-SEP-1996; 96WO-GB02382.

PR 27-SEP-1995; 95GB-0019737.

PA (PEPT-) PEPTIDE THERAPEUTIC LTD.

PI Elson CJ, Thompson JS;

DR WPI: 1997-212851/19.

PT Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis

PS Disclosure: Fig 1a; 91pp; English.

CC This peptide is one of a library (see AAM43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAM1948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.

SO Sequence 15 AA;

Query Match 55.2%; Score 48; DB 18; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAP 9
 |||||
 DB 7 VLEKKMGAP 15

RESULT 9

AAM43460
 ID AAM43460 standard; peptide: 16 AA.

AC AAM43460;

DT 08-APR-1998 (first entry)

DE Mycobacteria sp. hsp68 derived peptide (group 1 #10).

XX Heat shock protein; hsp58; autoimmune disease; hsp65; vaccine;
 KW rheumatoid arthritis; antigen; infectious disease; prophylactic;

KW pristane induced arthritis; PIA.
 XX
 OS Synthetic.
 OS Mycobacteria sp.
 XX
 PN MO9711966-A1.
 XX
 PD 03-APR-1997.
 XX
 PF 26-SEP-1996; 96WO-GB02382.
 XX
 PR 27-SEP-1995; 95GB-0019737.
 XX
 PA (PEPT-) PEPTIDE THERAPEUTIC LTD.
 XX
 PI Elson CJ, Thompson JS;
 XX
 DR WPI: 1997-212851/19.
 XX
 PS Polypeptide(s) derived from microbial heat shock protein - useful
 for treatment of autoimmune disease esp. arthritis
 PS Disclosure; Fig 1a; 91pp; English.
 XX
 CC This peptide is one of a library (see AAM43451-W43556) which represents
 CC the mycobacterial heat shock protein, hsp65 and is designed to study
 CC a novel method for the treatment of autoimmune disease e.g. rheumatoid
 CC arthritis. This fragment has been allocated as a group 1 peptide which
 CC is composed of the fragments found in AAM43451 to AAM43460. Mycobacterial
 CC hsp65 is known to be an immunodominant antigen in a number of infectious
 CC diseases and is linked to pristane induced arthritis (PIA) in vitro,
 CC however heat shock proteins and peptides derived from microbial sources
 CC may act as self antigens and thus have limited clinical use. The human
 CC hsp65 homologue, hsp58, or fragments of the hsp58 protein
 CC (see AAM14948-W14950) may be useful in the development of vaccines for
 CC prophylaxis or treatment of an autoimmune disease such as rheumatoid
 CC arthritis.
 XX
 SQ Sequence 16 AA:
 Query Match 44.8%; Score 39; DB 18; Length 16;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 PTITNDG 16
 DB 1 PTITNDG 7
 XX
 ULT 10
 AAR87908
 ID AAR87908 standard; peptide: 16 AA.
 XX
 AC AAR87908;
 XX
 DT 01-MAR-1996 (first entry)
 XX
 DE Bovine lactoferrin (24-39).
 XX
 KW antiviral; lactoferrin;
 XX
 OS Synthetic.
 XX
 PH Key
 FT Modified-site 1 Location/Qualifiers
 FT /note= "optionally this site is acetylated or
 FT preceded by a peptide"
 FT Modified-site 16
 FT /note= "optionally this site may be in amide form
 FT or followed by a peptide"
 XX
 PN JP07069915-A.
 XX

PD 14-MAR-1995.
 XX
 PF 02-SEP-1993; 93JP-0240284.
 XX
 PR 02-SEP-1993; 93JP-0240284.
 XX
 PA (SNOW) SNOW BRAND MILK PROD CO LTD.
 XX
 DR WPI: 1995-144726/19.
 XX
 PT Inhibitor against viral infection and proliferation - contains
 PT peptide having sequence from lactoferrin
 XX
 PS Claim 4; Page 2; 10pp; Japanese.
 XX
 CC The sequence is one of six peptides disclosed as having inhibitory
 CC effect against viral infection. The peptides are derived from
 CC lactoferrin. Their activity is demonstrated against cytomegalovirus.
 XX
 SQ Sequence 16 AA:
 Query Match 40.2%; Score 35; DB 16; Length 16;
 Best Local Similarity 77.8%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 5 KKGCAPTIT 13
 DB 4 KRLGAPSTI 12
 XX
 RESULT 11
 AAM10516
 ID AAM10516 standard; peptide: 16 AA.
 XX
 AC AAM10516;
 XX
 DT 02-APR-1997 (first entry)
 XX
 DE Lactoferrin derived antibacterial peptide.
 XX
 KW Lactoferrin; antibacterial; immunogen; monoclonal; antibody;
 KW human; bovine; hybridoma; sensitive; specific; detection;
 KW determination; gastric juice; intestine; faeces; blood; urine.
 XX
 OS Synthetic.
 XX
 PN JP08269099-A.
 XX
 PD 15-OCT-1996.
 XX
 PF 30-MAR-1995; 95JP-0073177.
 XX
 PR 30-MAR-1995; 95JP-0073177.
 XX
 PA (MORG) MORINAGA MILK IND CO LTD.
 XX
 DR WPI: 1996-515017/51.
 XX
 PT Monoclonal antibody combined with bovine or non-natural human
 PT lactoferrin fragment - for detecting lactoferrin-originated
 PT antibacterial peptide in e.g. gastric juice, urine etc
 XX
 PS Claim 3; Page 12; 13pp; Japanese.
 XX
 CC The present peptide is a lactoferrin (LF) derived antibacterial
 CC peptide, which can be used as an immunogen in the prepn. of a
 CC monoclonal antibody (MAB), capable of binding with a human or
 CC bovine LF fragment but not with natural LF, using standard
 CC hybridoma techniques. The MAB can be used for the highly sensitive
 CC and specific detection or determination of LF derived antibacterial
 CC peptides in gastric juice, intestinal contents, faeces, blood and
 CC urine.
 XX

SQ Sequence 16 AA:
Query Match 40.2%; Score 35; DB 17; Length 16;
Best Local Similarity 77.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 5 KKWGAPTT 13
111111
DB 2 KKLGAISIT 10

RESULT 12
AAR94782
ID AAR94782 standard; peptide: 16 AA.
XX
AC AAR94782;
XX
DT 11-NOV-1996 (first entry)
XX
XX Peptide from library spanning whole of hsp65.
XX
XX Hsp: heat shock protein; Mycobacterium bovis; microbial; diagnosis;
KM rheumatoid arthritis; autoimmune disease; treatment; vaccine;
KW prophylaxis.
XX
OS Synthetic.
XX
PN WO9610039-A1.
XX
PD 04-APR-1996.
XX
PF 27-SEP-1995; 95WO-GB02295.
XX
PR 27-SEP-1994; 94GB-0019553.
XX
PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX
PI Elson CJ, Thompson SJ;
XX
DR WPI: 1996-200888/20.
XX
XX Polypeptide derived from bacterial heat shock protein 65 - for use
PT in diagnosis, prophylaxis and treatment of auto-immune disease e.g.
PT rheumatoid arthritis.
XX
PS Example 1; Figure 1; 88pp; English.
XX
CC AAR94773-R94878 are overlapping peptides of a library spanning the
CC whole of microbial hsp65 (heat shock protein 65). Eleven antigens were
CC prepared from the library and used to immunise mice, after 10 days the
CC mice received injections of pristane to induce arthritis and the
CC animals examined for incidence of arthritis. A preferred anti-arthritis
CC peptide was found to correspond to residues 21-31 of full length hsp65
CC (see AAR94772). Peptides conty. this sequence are used in the diagnosis,
CC treatment and prophylaxis (may be used in a vaccine) of autoimmune
CC diseases such as rheumatoid arthritis.
XX
SQ Sequence 16 AA:
Query Match 39.1%; Score 34; DB 17; Length 16;
Best Local Similarity 85.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 10 PTITNDG 16
111111
DB 1 PTITNDG 7

RESULT 13
AAB90858
ID AAB90858 standard; peptide: 12 AA.
XX
AC AAB90858;

XX
DT 22-JUN-2001 (first entry)
XX
DE Melanocyte stimulating hormone (MSH) related peptide SEQ ID NO:30.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidy; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US13576.
XX
PR 17-MAY-1999; 99US-0134406.
PR 10-SEP-1999; 99US-0153406.
PR 15-OCT-1999; 99US-0159783.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;
XX
DR WPI: 2001-112059/12.
XX
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity
XX
PS Disclosure: Page 199; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (II) and a
CC reactive group (III) (e.g. succinimidy and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity
CC in vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention.
XX
SQ Sequence 12 AA:
Query Match 35.6%; Score 31; DB 22; Length 12;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 3 LEKKGAP 10
111111
DB 4 MEHRMGKP 11

RESULT 14
AAW14808
ID AAW14808 standard; peptide: 15 AA.
XX
AC AAW14808;
XX
DT 23-MAY-1997 (first entry)
XX
DE fes oncogene protein residues 674-688.
XX

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:12 : Search time 6.5 Seconds

(without alignments)
95.310 Million cell updates/sec

Title: US-09-847-637b-3

Sequence: 1 VLEKKWGPITNDG 16

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 814

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	28.7	13	1	MLA_ANOCA
2	25	28.7	13	1	P41589 anolis caro
3	25	28.7	13	1	P01198 camelus dro
4	24.5	28.2	15	1	UN01_PINPS
5	22	25.3	8	1	LCK_DROME
6	22	25.3	10	1	ACT_THUAL
7	20	23.0	13	1	UHA3_HUMAN
8	20	23.0	13	1	UN02_PINPS
9	19	21.8	10	1	MLB_SQUAC
10	19	21.8	12	1	BPP2_BOTJA
11	19	21.8	13	1	UP01_CAEEL
12	19	21.8	14	1	LIGA_TRAVE
13	19	21.8	14	1	SAP2_ARBP
14	18	20.7	10	1	BPP2_BOTIN
15	18	20.7	10	1	BPP8_BOTIN
16	18	20.7	12	1	BPP_VIPAS
17	18	20.7	13	1	PSP3_PHYPA
18	18	20.7	13	1	LIGA_TRAVE
19	18	20.7	13	1	PSBP_PINPS
20	18	20.7	13	1	TP13_PHYRO
21	17.5	20.1	5	1	MAIT_BACIN
22	17	19.5	6	1	BPP7_BOTIN
23	17	19.5	6	1	CIP2_MYRED
24	17	19.5	6	1	LOK1_LOCM1
25	17	19.5	8	1	LCK1_LEUMA
26	17	19.5	8	1	LCK2_LEUMA
27	17	19.5	8	1	LCK3_LEUMA
28	17	19.5	8	1	LCK4_LEUMA
29	17	19.5	8	1	LCK5_LEUMA
30	17	19.5	8	1	LCK6_LEUMA
31	17	19.5	8	1	LCK7_LEUMA
32	17	19.5	9	1	LCK8_LEUMA
33	17	19.5	10	1	FAR6_ASCSU
					P82660 panagrellus

34	17	19.5	10	1	HFP1_ROMMI	P18110 romalea mic
35	17	19.5	10	1	HFP2_CARMO	P11385 carexusius m
36	17	19.5	10	1	HFP_HELZE	P16353 heliothis z
37	17	19.5	10	1	HFP_NAUCI	P10939 nauphoeta c
38	17	19.5	10	1	HFP_TABAT	P14596 tabanus atr
39	17	19.5	10	1	LABA_JATMU	P13270 jatropha mu
40	17	19.5	10	1	LPR2_LOCM1	P41488 locusta mig
41	17	19.5	10	1	UPA9_HUMAN	P30095 homo sapien
42	17	19.5	13	1	IDHP_RAT	P56574 rattus norv
43	17	19.5	15	1	PKB7_PINPS	P81104 pinus pins
44	17	19.5	15	1	PDGB_PIG	P20034 sus scrofa
45	17	19.5	15	1	RKCG_CARCR	P21586 caretta car

ALIGNMENTS

```

RESULT 1
MLA_ANOCA          STANDARD:      PRT:      13 AA.
AC  P41589:
DT  01-NOV-1995 (Rel. 32, Created)
DT  01-NOV-1995 (Rel. 32, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Melanotropin alpha (Alpha-MSH).
OS  Anolis carolinensis (Green anole) (American chameleon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Lepidosauria; Squamata; Iguania; Iguanidae; Polychrotidae; Anolis.
OX  NCBI_TaxID=28377;
RN  [1]
RP  TISSUE= pituitary;
RC  MEDLINE=92270473; PubMed=1667689;
RA  Dorez R.M., Lancha A., Rand-weaver M., Jankelow L., Adamczyk D.L.;
RT  "Detection of a novel sequence change in the major form of alpha-MSH
RT  isolated from the intermediate pituitary of the reptile, Anolis
RT  carolinensis.";
RL  Peptides 12:1261-1266(1991).
CC  -1 SIMILARITY: BELONGS TO THE POMC FAMILY.
KW  Hormone; Amidation.
FT  MOD_RES      13
SQ  SEQUENCE      13 AA; 1608 MW; FF990A7358BB09C1 CRC64;

Query Match
Best Local Similarity 28.7%; Score 25; DB 1; Length 13;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY  6 KMGAP 10
DB  8 RMGKP 12

RESULT 2
MLA_CAMDR          STANDARD:      PRT:      13 AA.
AC  P01198:
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Melanotropin alpha (Alpha-MSH).
OS  Camelus dromedarius (Dromedary) (Arabian camel), and
OS  Equus caballus (Horse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX  NCBI_TaxID=9838, 9796;
RN  [1]
RP  SPECIES=C. dromedarius;
RC  MEDLINE=75146434; PubMed=1125179;
RA  Li C.H., Danno W.O., Chung D., Rao A.J.;
RT  "Isolation, characterization, and amino acid sequence of
RT  melanotrophin from camel pituitary glands.";
RL  Biochemistry 14:947-952(1975).

```

FN	[2]	SEQUENCE.				
RP		SPECIES=HORSE; TISSUE=Pituitary;				
RC		Dixon J.S., Li C.H.:				
RA		"The isolation and structure of alpha-melanocyte-stimulating hormone				
RT		from horse pituitaries."				
RT		J. Am. Chem. Soc. 82:4568-4572(1960).				
RL		-I- SIMILARITY: BELONGS TO THE POMC FAMILY.				
CC		PIR: A01464; MTCMAD.				
DR		PIR: A91785; MTHOAD.				
KW		Hormone; Acetylation; Amidation.				
FT	MOD_RES	1	ACETYLATION (IN ABOUT 50% OF CAMEL			
FT			MOLECULES).			
FT			AMIDATION.			
SO	MOD_RES	13				
	SEQUENCE	13 AA; 1624 MW;	FF991CA958BB09C1 CRC64;			
	Query Match	28.7%;	Score 25; DB 1; Length 13;			
	Best Local Similarity	60.0%;	Pred. No. 4, 1e+02;			
	Matches 3; Conservative	1; Mismatches 1; Indels	0; Gaps	0;		
	6 KWGAP 10					
	8 RWGAP 12					

```

RESULT 3
UN01_PINPS
ID UN01_PINPS STANDARD: PRT; 15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Unknown protein from 2D-page of needles (S1247/S1248) (N150/N151)
DE (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RA Plomion C., Costa P., Bahrman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. I. Mapping
RT dominant and codominant protein markers assayed on diploid tissue, in
RT a haploid-based genetic map."
RL Silvae Genetica 46:161-165(1997).
RN [2]
RF SEQUENCE.
RQ TISSUE=Needle;
RZ MEDLINE=99274088; PubMed=10344291;
RA Costa P., Plomionau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -I- MISCELLANEOUS: ON THE 2D-GEL,THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.5, ITS MW IS: 62 kDa.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match 28.7%; Score 25; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 4.7e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 EKKWCAPTIND 15
::: |::|
Db 2 EQGTOPSATND 13

RESULT 4
LCK_DROME STANDARD: PRT; 15 AA.

```

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CC      P81829; 2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Leucokinin (DLK).
GN      pp OR DLK.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
RN      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Neurosecretory cell;
RX      MEDLINE=20044845; PubMed=10574744;
RA      Tenzhaz S., O'Connell F.C., Pollock V.P., Kean L., Davies S.A.,
RA      Veenstra J.A., Dow J.A.T.;
RT      "Isolation and characterization of a leucokinin-like peptide of
RT      Drosophila melanogaster."
RL      J. Exp. Biol. 202;3667-3676(1999).
RN      [2]
RP      SEQUENCE FROM N.Y.
RC      STRAIN=BERKELEY.
RA      Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazey R.G.,
RA      Butenoff C., Champe M., Chavez C., Chew M., Gieslioka L., Doyle C.M.,
RA      Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA      Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA      Lewis S., Li P., Lumotani M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA      Nixon K., Paolel J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA      Setliff H., Snir E., Svirska R.R., Wan K.H., Weinburg T., Zhang R.,
RA      Zieran L.B., Rubin G.M.;
RL      submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE
CC      SECRETATE CELLS TO RAISE CHLORIDE CONDUCTANCE.
-----
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-----
DR      EMBL; AC006496; -; NOT_ANNOTATED_CDS.
DR      FlyBase; FBgn0028418; Leucokinin.
RW      Neuropeptide; Amidation.
FT      MOD_RES 15 15 AMIDATION.
SQ      SEQUENCE 15 AA; 1743 MW; 4793A08F251C9525 CRC64;

Query Match 28.2%; Score 24.5; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. NO. 5.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Yy 1 VLEKK-----WG 8
    ||| ||| |||
Db 3 VVLGKKQRFHSMG 15

RESULT 5
ACI_THUAL
AC PI8691; STANDARD; PRT; 8 AA.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacar (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
XN NCBI_TaxID=8236;
XN [1]
```

```

RA Raftan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
RA Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Paelel J.M., Park S., Pfeiffer B., Poon L., Sequelra A.,
RA Seethi H., Snir E., Svirskaas R.R., Wan K.H., Weinburg T., Zhang R.,
RA Zierman L.L., Rubin G.M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: ACTS THROUGH INTRACELLULAR CALCIUM IN MALPIGHIAN TUBULE
CC STELLATE CELLS TO RAISE CHLORIDE CONDUCTANCE.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AC006496; ?; NOT_ANNOTATED_CDS.
DR FlyBase; FBgn0028418; leucokinin.
KW Neuropeptide; Amidation.
FT MOD_RRS 15
FT SEQUENCE 15 AA; 1743 MW; 4793A08F251C9525 CRC64;
QY 1 VLEKK-----WG 8
Db 3 VVLGKKRFHSMG 15
Query Match 28.2%; Score 24.5; DB 1; Length 15;
Best Local Similarity 53.8%; Pred. No. 5.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

RESULT 5
ACI_THOVAL
ACI_THOVAL STANDARD; PRT; 8 AA.
AC P18691;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 01-NOV-1990 (Rel. 16, Last annotation update)
DE Angiotensin-converting enzyme inhibitor.
OS Thunnus albacares (Yellowfin tuna) (Neothunnus macropterus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Scombroidei;
OC Scombridae; Thunnus.
OX NCBI_TaxID=8236;
NN [1]

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:39:33 : Search time 20 seconds

(without alignments)
138.396 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKWGAPITNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

11 number of hits satisfying chosen parameters: 3277

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	25	28.7	10 11 070580	070580 mus muscula
2	25	28.7	15 9 038427	038427 bacterioph
3	25	28.7	16 2 045530	045530 bacillus su
4	25	28.7	16 4 09UCR9	09UCR9 homo sapien
5	24	27.6	11 4 060842	060842 homo sapien
6	24	27.6	14 2 047599	047599 escherichia
7	23	26.4	11 2 P83147	P83147 bacterioides
8	23	26.4	11 15 083410	083410 mouse mamma
9	23	26.4	13 15 085645	085645 mouse mamma
10	23	26.4	16 2 010748	010748 clostridium
11	23	26.4	16 4 09UC18	09UC18 homo sapien
12	23	26.4	16 10 09S8D6	09S8D6 triticum ae
13	22	25.3	12 15 098240	098240 human immun
14	22	25.3	13 16 09K9D7	09K9D7 bacillus ha
15	22	25.3	15 8 093386	093386 sus scrofa
16	21	24.1	8 8 094VB5	094VB5 varanus sal

17	21	24.1	8 8 094VB2	094VB2 varanus sal
18	21	24.1	8 8 094VA7	094VA7 varanus sal
19	21	24.1	8 8 094PX7	094PX7 felis silve
20	21	24.1	8 8 094PX6	094PX6 felis libyc
21	21	24.1	8 8 094PX5	094PX5 felis silve
22	21	24.1	9 8 094VC6	094VC6 varanus pil
23	21	24.1	10 8 094VDS	094VDS varanus cil
24	21	24.1	13 8 09MOK6	09MOK6 rupicapra r
25	21	24.1	13 8 09MOK3	09MOK3 capra libex
26	21	24.1	13 8 09MOK0	09MOK0 cervus elap
27	21	24.1	14 12 P91578	P91578 chorisioleu
28	21	24.1	15 4 09BXX4	09BXX4 homo sapien
29	21	24.1	15 8 P92076	P92076 euhadra her
30	21	24.1	16 4 014495	014495 homo sapien
31	21	24.1	16 5 09NFW0	09NFW0 trypanosoma
32	20	23.0	11 2 09EUC3	09EUC3 escherichia
33	20	23.0	13 4 050831	050831 methanococc
34	20	23.0	13 4 014462	014462 homo sapien
35	20	23.0	15 6 09FS39	09FS39 gorilla gor
36	20	23.0	15 10 09S914	09S914 hordeum vul
37	20	23.0	16 1 P72023	P72023 methanosarc
38	20	23.0	16 4 09UC10	09UC10 homo sapien
39	20	23.0	16 6 09TRD1	09TRD1 sus scrofa
40	19	21.8	8 8 094V82	094V82 varanus yuw
41	19	21.8	10 5 09TWU1	09TWU1 fusinus fer
42	19	21.8	10 6 09FS42	09FS42 sus scrofa
43	19	21.8	12 7 077879	077879 oreochromis
44	19	21.8	12 12 084268	084268 human papil
45	19	21.8	13 2 048357	048357 escherichia

ALIGNMENTS

RESULT 1
ID 070580 PRELIMINARY; PRT; 10 AA.
AC 070580:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE III (FRAGMENT).
GN CAR3 OR CAR5 OR CA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene.";
RL Gene 214:157-165(1999).
DR EMBL, AJ006474; CAA07057.1; -
DR MGD; MGI:1351477; Cars.
DR MGD; MGI:88270; Car3.
FT NON_TER
SQ SEQUENCE 10 AA; 1105 MW; 56F7FE71ADC37B13 CRC64;
Query Match 28.7%; Score 25; DB 11; Length 10;
Best Local Similarity 37.5%; Pred. No. 1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 LEKKWGAP 10
DB 1 MAKEWATP 8
RESULT 2
ID 038427 PRELIMINARY; PRT; 15 AA.
AC 038427:
DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CORE PROTEIN (FRAGMENT).
OS Bacteriophage T4.
OC Bacteriophage T4.
OC dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like phages.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85083058; PubMed=6512858;
RA Keller B., Sengstag C., Kellenberger E., Bickie T.A.;
RT "Gene 68, a new bacteriophage T4 gene which codes for the 17K prohead
core protein is involved in head size determination."
RL J. Mol. Biol. 179:415-430(1984).
DR EMBL; X01414; CAA25657.1; -
FT NON_TER
SQ SEQUENCE 15 AA; 1713 MW; 1B455B28262C0229 CRC64;

Query Match 28.7%; Score 25; DB 9; Length 15;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 VLEKKWGAP 10
DB 6 LLETWGKP 14

RESULT 3

045530 PRELIMINARY; PRT; 16 AA.

AC 045530;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE CHLORAMPHENICOL ACETYLTRANSFERASE (EC 2.3.1.28) (FRAGMENT).
GN CAR.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168; TRANSPOSON=TN9;
RC MEDLINE=85113144; PubMed=2982142;
RA Lin C.K., Goldfarb D.S., Doi R.H., Rodriguez R.L.;
RT "Mutations that affect the translation efficiency of Tn9-derived cat
RT gene in Bacillus subtilis."
RL Proc. Natl. Acad. Sci. U.S.A. 82:173-177(1985).
FT NON_TER
SQ SEQUENCE 16 AA; 1936 MW; B4894C04C5A5409F CRC64;

Query Match 28.7%; Score 25; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 3 LEKKWGAPTI 12
DB 1 MEKKIGYTTV 10

RESULT 4

09UCK9 PRELIMINARY; PRT; 16 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE SERUM AMYLOID A ISOTYPE 2 ALPHA PROTEIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93099171; PubMed=1463770;
RA Baba S., Takahashi T., Kasama T., Shirasawa H.;
RT "Identification of two novel amyloid A protein subsets coexisting in
an individual patient of AA-amyloidosis."
RL Blochim. Biophys. Acta 1180:195-200(1992).
DR InterPro; IPR000096; Serum_amyloid_A.
DR Pfam; PF00277; SAA_proteins; 1.
SQ SEQUENCE 16 AA; 1612 MW; 1CAB4F077C9C8C01 CRC64;

Query Match 28.7%; Score 25; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 WCAPITTN 14
DB 7 WAAEVISN 14

RESULT 5

060842 PRELIMINARY; PRT; 11 AA.

AC 060842;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE (FRAGMENT).
GN CA3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Sowden J., Smith H., Morrison K., Edwards Y.;
RT "Sequence comparisons and functional studies of the proximal promoter
RT of the carbonic anhydrase 3 (CA3) gene."
RL Gene 214:157-165(1999).
DR EMBL; AJ006473; CAA07056.1; -
FT NON_TER
SQ SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 27.6%; Score 24; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 LEKKWG 8
DB 1 MAKWNG 6

RESULT 6

047599 PRELIMINARY; PRT; 14 AA.

DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE C (FRAGMENT).
GN C.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:42:03 : Search time 10.5 Seconds
(without alignments)
37.220 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKMGAPITNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

1 number of hits satisfying chosen parameters: 106182

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCtus.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	36.8	10	4	US-08-687-590-67
2	30	34.5	14	4	US-08-584-043A-80
3	30	34.5	16	4	US-08-602-999A-228
4	30	34.5	16	4	US-08-030-410-1
5	27	31.0	7	4	US-08-687-590-72
6	27	31.0	9	1	US-08-452-083-23
7	27	31.0	9	1	US-08-468-557-12
8	27	31.0	10	2	US-08-556-597-158
9	27	31.0	15	1	US-07-907-190-8
10	27	31.0	15	1	US-08-320-373-37
11	27	31.0	15	3	US-08-491-954-9
12	26	29.9	6	4	US-08-893-654B-15
13	26	29.9	8	2	US-08-621-803-237
14	26	29.9	8	2	US-08-621-259A-239
15	26	29.9	8	2	US-08-621-259A-243
16	26	29.9	8	4	US-09-296-284-14
17	26	29.9	8	4	US-09-217-352-237
18	26	29.9	10	2	US-08-556-597-145
19	26	29.9	10	2	US-08-556-597-152
20	26	29.9	11	1	US-08-346-849-23
21	26	29.9	11	6	US-08-293-284A-23
22	26	29.9	11	6	US-08-293-284A-23
23	26	29.9	12	1	US-07-778-233B-36
24	26	29.9	12	1	US-07-963-321-36
25	26	29.9	12	1	US-08-290-641-36
26	26	29.9	12	1	US-08-548-540-36
27	26	29.9	12	5	PCT-US96-09809-36

28	26	29.9	15	1	US-08-111-939-10	Sequence 10, Appl
29	26	29.9	16	1	US-08-307-724B-21	Sequence 21, Appl
30	26	29.9	16	4	US-09-242-131A-11	Sequence 11, Appl
31	26	29.9	16	4	US-09-615-283-11	Sequence 11, Appl
32	25	28.7	6	3	US-08-472-595-6	Sequence 6, Appl1
33	25	28.7	6	3	US-08-207-575A-6	Sequence 6, Appl1
34	25	28.7	6	3	US-08-246-441-15	Sequence 15, Appl
35	25	28.7	7	4	US-08-946-525-10	Sequence 10, Appl
36	25	28.7	9	1	US-08-452-083-24	Sequence 24, Appl
37	25	28.7	9	1	US-08-468-557-14	Sequence 14, Appl
38	25	28.7	9	2	US-08-751-767A-65	Sequence 65, Appl
39	25	28.7	10	1	US-08-671-525B-19	Sequence 19, Appl
40	25	28.7	10	1	US-08-672-109B-19	Sequence 19, Appl
41	25	28.7	10	2	US-08-842-045-19	Sequence 19, Appl
42	25	28.7	10	2	US-08-842-238-19	Sequence 19, Appl
43	25	28.7	10	3	US-08-629-335B-19	Sequence 19, Appl
44	25	28.7	11	3	US-08-916-443A-1	Sequence 1, Appl1
45	25	28.7	11	3	US-08-916-913A-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-08-687-590-67
Sequence 67, Application US/08687590
Patent No. 6255070
GENERAL INFORMATION:
APPLICANT: Willison, Keith Robert
APPLICANT: Kubota, Hiroshi
APPLICANT: Ashworth, Alan
TITLE OF INVENTION: Folding Proteins
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,590
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00192
FILING DATE: 31-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9418234.2
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084619-000000US
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-687-590-67
Query Match 36.8%; Score 33; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 11 TITNDG 16
111111
Db 1 TITNDG 6

RESULT 2

US-08-584-043A-80
; Sequence 80, Application US/08584043A
; Patent No. 6344436
; GENERAL INFORMATION:
; APPLICANT: Smith, Louis C.
; APPLICANT: Sparrow, James T.
; APPLICANT: Hauer, Jochen
; APPLICANT: Mims, Martha P.
; TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
; TITLE OF INVENTION: MACROMOLECULE DELIVERY
; NUMBER OF SEQUENCES: 139
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; OPERATING SYSTEM: IBM P.C. DOS 6.0
; SOFTWARE: Word Perfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584, 043A
; FILING DATE: January 8, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 217/189
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELETYPE: 67-3510
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-584-043A-80

Query Match 34.5%; Score 30; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 LEKRW 7
111111
Db 5 LEKRW 9

RESULT 3

US-08-602-999A-228
; Sequence 228, Application US/08602999A
; Patent No. 6184205
; GENERAL INFORMATION:
; APPLICANT: SPARKS, Andrew B.
; APPLICANT: KAY, Brian K.
; APPLICANT: THORN, Judith M.

APPLICANT: OUILLIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602, 999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8664
TELETYPE: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 228:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-602-999A-228

Query Match 34.5%; Score 30; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 KWGAP 10
111111
Db 1 RWGAP 5

RESULT 4

US-08-030-410-1
; Sequence 1, Application US/08030410
; Patent No. 6221359
; GENERAL INFORMATION:
; APPLICANT: Komiyama, Atsushi
; APPLICANT: Nakahata, Tatsutoshi
; APPLICANT: Kubo, Tetsuo
; APPLICANT: Tanaka, Ryuhel
; APPLICANT: Kawano, Genji
; APPLICANT: Sudo, Tetsuo
; APPLICANT: Sano, Emiko
; APPLICANT: Kojima, Katsunaki
; TITLE OF INVENTION: HEMOPHILIC STEM CELL MULTIPLIER
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 10.6667 Seconds

(without alignments)
144.134 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKWGAPITINDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

1 number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: PIR_71.*
2: PIR1.*
3: PIR2.*
4: PIR3.*
5: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	540	2 A26950	groEL2 protein - M
2	87	100.0	540	2 A43509	65K antigen mba -
3	87	100.0	540	2 C41325	heat shock protein
4	87	100.0	541	2 S40245	heat shock protein
5	87	100.0	541	2 T44725	chaperonin 60K (im
6	87	100.0	588	2 A25902	65K antigen - Myco
7	77	88.5	538	2 H72367	groEL protein - Th
8	72	82.8	540	2 S37566	groEL protein - S
9	72	82.8	540	2 B41325	heat shock protein
10	71	81.6	541	2 T35591	chaperonin cpn60 -
11	71	81.6	541	2 S72614	chaperonin 60 - Th
12	68	78.2	538	2 J01195	heat shock protein
13	68	78.2	539	2 B49855	heat shock protein
14	68	78.2	542	2 A01704	class I heat-shock
15	68	78.2	542	2 A01333	class I heat-shock
16	68	78.2	543	2 B41872	heat shock protein
17	68	78.2	543	2 F97232	chaperonin GroEL,
18	68	78.2	544	2 J05130	heat shock protein
19	68	78.2	544	2 B41884	58K heat shock pro
20	68	78.2	544	2 J06063	chaperonin groEL -
21	68	78.2	544	2 B83720	class I heat-shock
22	67	77.0	543	2 S70013	chaperonin-like pr
23	66	75.9	528	2 S73270	chaperonin, 60K -
24	66	75.9	541	2 T06829	chaperonin groEL -
25	66	75.9	541	2 A62263	chaperonin groEL -
26	66	75.9	546	2 S34938	heat shock protein
27	66	75.9	548	2 G75499	groEL protein - De
28	66	75.9	550	2 A41468	60K heat shock pro
29	66	74.7	541	2 S68249	chaperonin groEL h

30	65	74.7	544	1 BVCGL	chaperonin groEL -
31	65	74.7	546	2 B47073	chaperonin GroEL -
32	64	73.6	539	2 S22342	chaperonin HSP60 -
33	64	73.6	542	2 J06061	heat shock protein
34	64	73.6	542	2 S32106	groEL protein - La
35	64	73.6	542	2 B86674	chaperonin, 60 kDa
36	63	72.4	540	2 G95222	chaperonin, 60 kDa
37	63	72.4	540	2 H98086	chaperonin GroEL, I
38	63	72.4	544	2 B82048	chaperonin, 60 kD
39	63	72.4	547	2 J04519	chaperonin, 60 kD
40	63	72.4	547	2 B43606	heat shock protein
41	63	72.4	547	2 B49203	heat shock protein
42	63	72.4	547	2 B83098	groEL protein PA43
43	63	72.4	548	1 BVCGL	chaperonin groEL -
44	63	72.4	548	2 D91269	chaperonin groEL I
45	63	72.4	548	2 B86110	hypothetical prote

ALIGNMENTS

```
RESULT 1
A26950
groEL2 protein - Mycobacterium tuberculosis (strain H37RV)
M:Alternate names: 65K antigen
C:Species: Mycobacterium tuberculosis
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 20-Jun-2000
C:Accession: A26950; A70830
R:Shinnick, T.M.
J: Bacteriol. 169, 1080-1088, 1987
A:Title: The 65-kilodalton antigen of Mycobacterium tuberculosis.
A:Reference number: A26950; MUID:87137260
A:Accession: A26950
A:Molecule type: DNA
A:Residues: 1-540 <SH1>
A:Cross-references: GB:M15467; NID:g149999; PIDN:AAA8232.1; PID:g150000
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon
Comor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno
A:Reference number: A70500; MUID:98295987
A:Accession: A70830
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-540 <CO1>
A:Cross-references: GB:AL021932; GB:AL123456; NID:g3261527; PIDN:CAA17397.1; PID:g290
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: groEL2; RV0440
C:Superfamily: chaperonin groEL
Query Match
Best Local Similarity 100.0%; Score 87; DB 2; Length 540;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 VVLEKKWGAPITINDG 16
Db 37 VVLEKKWGAPITINDG 52
RESULT 2
A43509
65K antigen mba - Mycobacterium bovis
C:Species: Mycobacterium bovis
C:Date: 28-Oct-1992 #sequence_revision 28-Oct-1992 #text_change 26-Aug-1999
C:Accession: A43509
R:Phole, J.E.R.; Keulen, W.J.; Kolk, A.H.J.; Groothuis, D.G.; Bernald, L.G.; Tiesjema
Infect. Immun. 55, 1466-1475, 1987
A:Title: Characterization, sequence determination, and immunogenicity of a 64-kilodal
A:Reference number: A43509; MUID:87193155
A:Accession: A43509
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A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-540 <THO>
A:Cross-references: GB:M17705; NID:g149933; PIDN:AAA5358.1; PID:g149934
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VLEKKMGAPTTNDG 16
DB 37 VLEKKMGAPTTNDG 52

RESULT 3

C41325
heat shock protein 56 - Streptomyces albus
N:Alternate names: heat shock protein groEL homolog 2
C:Species: Streptomyces albus
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 26-Aug-1999
C:Accession: C41325
R:Mazodier, P.; Guglielmi, G.; Davies, J.; Thompson, C.J.
J. Bacteriol. 173:7382-7386, 1991
A:Title: Characterization of the groEL-like genes in Streptomyces albus.
A:Reference number: A41325; MUID:92041639
A:Accession: C41325
A:Molecule type: DNA
A:Residues: 1-540 <MAZ>
A:Cross-references: GB:M76658; NID:g153293; PIDN:AAA26754.1; PID:g153294
C:Genetics:
A:Gene: groEL2
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VLEKKMGAPTTNDG 16
DB 37 VLEKKMGAPTTNDG 52

RESULT 4

S40245
heat shock protein 65 - Mycobacterium paratuberculosis
C:Species: Mycobacterium paratuberculosis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-Aug-1999
C:Accession: S40245
R:Walston, X.Y.Z.; McConnell, X.Y.Z.; Bujdosó, R.
submitted to the EMBL Data Library, August 1993
A:Description: Cloning and expression of Mycobacterium paratuberculosis HSP65KD.
A:Reference number: S40245
A:Accession: S40245
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <COL>
A:Cross-references: EMBL:X74518; NID:g438180; PIDN:CAA52630.1; PID:g438181
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAPTTNDG 16
DB 37 VLEKKMGAPTTNDG 52

RESULT 5

T44725
chaperonin 6CK [imported] - Mycobacterium leprae
N:Alternate names: heat shock protein GroEL-2

C:Species: Mycobacterium leprae
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T44725
R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, January 1998
A:Reference number: Z22831
A:Accession: T44725
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-541 <JAM>

A:Cross-references: EMBL:AL035159; PIDN:CAA22689.1
A:Experimental source: cosmid B1450
C:Genetics:
A:Gene: groEL-2
C:Superfamily: chaperonin groEL
C:Keywords: molecular chaperone

Query Match 100.0%; Score 87; DB 2; Length 541;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKMGAPTTNDG 16
DB 37 VLEKKMGAPTTNDG 52

RESULT 6

A25902
65K antigen - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 12-Sep-1997
C:Accession: A25902
R:Mehra, V.; Sweetser, D.; Young, R.A.
Proc. Natl. Acad. Sci. U.S.A. 83:7013-7017, 1986
A:Title: Efficient mapping of protein antigenic determinants.
A:Reference number: A25902; MUID:86313701
A:Accession: A25902
A:Molecule type: DNA
A:Residues: 1-588 <MEH>
C:Superfamily: chaperonin groEL

Query Match 100.0%; Score 87; DB 2; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VLEKKMGAPTTNDG 16
DB 84 VLEKKMGAPTTNDG 99

RESULT 7

H72367
groEL protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: H72367
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399: 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A:Reference number: A72200; MUID:99287316
A:Accession: H72367
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-538 <ARN>
A:Cross-references: GB:AE001727; GB:AE000512; NID:g4981015; PIDN:AAD35591.1; PID:g498
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0506
C:Superfamily: chaperonin groEL

Query Match 88.5%; Score 77; DB 2; Length 538;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:01 : Search time 5.62963 Seconds
(without alignments)
110.045 Million cell updates/sec

Title: US-09-847-637b-3

Sequence: 1 VLEKKWKGAPTTNDG 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

1 number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	87	100.0	476	1 CH62_STRLI	033658 streptomyc
2	87	100.0	539	1 CH62_MYCTU	P06868 streptococ
3	87	100.0	539	1 CH62_STRAL	Q00768 streptomyc
4	87	100.0	540	1 CH60_MYCPA	P42384 mycobacteri
5	87	100.0	540	1 CH62_MYCLE	P09239 mycobacteri
6	77	88.5	538	1 CH60_THEMA	Q9wyx6 thermotoga
7	72	82.8	539	1 CH61_STRAL	Q00767 streptomyc
8	72	82.8	540	1 CH61_STRCO	P40171 streptomyc
9	71	81.6	540	1 CH60_THERB	Q60024 thermotoga
10	68	78.2	538	1 CH60_BACP3	P26209 bacillus st
11	68	78.2	539	1 CH60_BACST	Q07201 bacillus st
12	68	78.2	542	1 CH60_THERH	P45746 thermus aqu
13	68	78.2	543	1 CH60_BACSV	P28598 bacillus su
14	68	78.2	543	1 CH60_CLOAB	Q50305 bacillus ha
15	68	78.2	544	1 CH60_BACHD	P30717 clostridium
16	67	77.0	540	1 CH61_STRLI	Q57002 streptomyc
17	67	77.0	543	1 CH62_SYNVU	P51349 porphyra pu
18	66	75.9	528	1 CH60_PORPU	Q37757 cyanophora
19	66	75.9	541	1 CH60_CYAPA	O50323 synchococc
20	66	75.9	544	1 CH61_SYNVU	P35468 leptospira
21	66	75.9	546	1 CH60_LEPIN	P26878 legionella
22	66	75.9	547	1 CH60_LEPIN	O33500 pseudomonas
23	66	75.9	552	1 CH60_PSEST	P12834 synchococc
24	65	74.7	300	1 CH60_SYNP6	P48212 clostridium
25	65	74.7	540	1 CH60_CLOFM	P22879 synchococc
26	65	74.7	544	1 CH60_SYNP7	P31293 chromatiu
27	65	74.7	546	1 CH60_CHRYI	O78419 guillardia
28	64	73.6	529	1 CH60_GUTHI	P26821 clostridium
29	64	73.6	539	1 CH60_CLOPE	P37282 lactococcus
30	64	73.6	542	1 CH60_LACLA	O66200 enterobacte
31	63	72.4	539	1 CH60_ENTAG	O66196 enterobacte
32	63	72.4	539	1 CH60_ENTAM	O66190 enterobacte
33	63	72.4	539	1 CH60_ENTAS	

34	63	72.4	539	1 CH60_ENTIT	O66192 enterobacte
35	63	72.4	539	1 CH60_SERRU	O66202 serratia ru
36	63	72.4	540	1 CH60_ENTAE	O66198 enterobacte
37	63	72.4	540	1 CH60_ENTGE	O66194 enterobacte
38	63	72.4	540	1 CH60_ERMAP	O66220 erwiniaph
39	63	72.4	540	1 CH60_ERWCA	O66214 klebsiella
40	63	72.4	540	1 CH60_KLEON	O66210 klebsiella
41	63	72.4	540	1 CH60_KLEOX	O66210 klebsiella
42	63	72.4	540	1 CH60_KLEPL	O66212 klebsiella
43	63	72.4	540	1 CH60_SERFI	O66204 serratia fi
44	63	72.4	540	1 CH60_SERMA	O66206 serratia ma
45	63	72.4	541	1 CH60_ERWHE	O66216 erwiniapher

ALIGNMENTS

RESULT 1

ID	CH62_STRLI	STANDARD:	PRT:	476 AA.
AC	O33658:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	60 kDa chaperonin 2 (Protein Cpn60 2) (GroEL2 protein).			
GN	GROEL2 OR GROEL2.			
OS	Streptomyces lividans.			
OC	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;			
OC	Actinomycetales; Streptomycetales; Streptomycetaceae; Streptomyces.			
OX	NCBI_TaxID=1916;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=TK21;			
RA	MEDLINE=98048481; PubMed=9387235;			
RA	de Leon P., Marco S., Islegas C., Marina A., Carrasosa J.L.,			
RA	Mellado R.P.;			
RT	*Streptomyces lividans groEL and groEL2 genes.*;			
RL	Microbiology 143:3563-3571(1997).			
CC	- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND			
CC	PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS			
CC	CONDITIONS (BY SIMILARITY).			
CC	- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF			
CC	7 SUBUNITS (BY SIMILARITY).			
CC	- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	EMBL: X95971; CA65226.1; -			
DR	HSSP: P45746; ISRV.			
DR	InterPro: IPR001844; Chaperonins_cpn60.			
DR	InterPro: IPR002423; TCPL_cpn60.			
DR	Pfam: PF00118; cpn60_TCP1.1.			
DR	PRINTS: PRO0298; CHAPERONIN60.			
DR	PRINTS: PRO0304; TCOMPLEXTCP1.			
DR	PROSITE: PS00326; CHAPERONINS_CPN60.1.			
KW	Chaperone; ATP-binding; Multigene family.			
FT	INT_MET 0			
FT	SEQUENCE 476 AA: 50529 MW: 76081793f4FED4D CRC64;			

Query Match

Best local similarity 100.0%; Score 87; DB 1; Length 476;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKWKGAPTTNDG 16
DB 36 VLEKKWKGAPTTNDG 51

```

RESULT 2
CH62_MYCNU
ID CH62_MYCTU STANDARD: PRT: 539 AA.
AC P06806; Q48931; Q48920;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60-2) (groEL protein 2) (65 kDa antigen) (Heat shock protein 65) (Cell wall protein A) (Antigen A).
GN GROEL2 OR GROEL2 OR GROEL-2 OR HSP65 OR RV0440 OR MT0456 OR MT037.04.
OS Mycobacterium tuberculosis, and
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=ERDMANN;
MD MEDLINE=87137260; PubMed=3029018;
RT Shinnick T.M.;
RT "The 65-kilodalton antigen of Mycobacterium tuberculosis.";
RL J. Bacteriol. 169:1080-1088(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
MD MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eigmeier K., Gas S., Barry C.E. III, Tenaka F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S., Hornsby T., Jagels K., Kellwell T., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sutton J.E., Taylor K., Whitehead S., Barrell B.G.;
RA "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
RT Nature 393:537-544(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O., Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E., Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A., Bishai W.;
RA "Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=BCG;
MD MEDLINE=87193155; PubMed=3553003;
RA Thole J.E.R., Keulen W.J., Kolk A.H.J., Groothuis D.G., Bernald L.G., Tiesjema R.H., van Embden J.D.A.;
RA "Characterization, sequence determination, and immunogenicity of a 64-kilodalton protein of Mycobacterium bovis BCG expressed in Escherichia coli K-12.";
RT Infect. Immun. 55:1466-1475(1987).
RN [5]
RP SEQUENCE OF 45-195 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=356, AND 12-14001;
RA Ros C., Belak K.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 63-182 FROM N.A.
RC SPECIES=M.bovis, and M.tuberculosis; STRAIN=TMCA10, AND TMCI024;
MD MEDLINE=95150784; PubMed=7848059;
RA Kapur V., Li L.L., Hamrick M.R., Plakayis B.B., Shinnick T.M., Rajendran A., Jacobs W.R. Jr., Banerjee A., Cole S., Yuen K.Y., Claridge J.E., Kreiswirth B.N., Musser J.M.;
RA "Rapid Mycobacterium species assignment and unambiguous identification of mutations associated with antimicrobial resistance

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RT in Mycobacterium tuberculosis by automated DNA sequencing.";
RL Arch. Pathol. Lab. Med. 119:131-138(1995).
RN [7]
RP SEQUENCE OF 64-177 FROM N.A.
RC SPECIES=M.tuberculosis;
MD MEDLINE=95214306; PubMed=7699930;
RA Hidaka E., Ueno I., Kawakami Y., Furuwatari C., Furihata K., Katsuyama T.;
RA "Detection and identification of mycobacteria by PCR-RFLP method.";
RT Risho Biory 43:155-161(1995)
RN [8]
RP FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS (BY SIMILARITY).
CC -1 SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF 7 SUBUNITS (BY SIMILARITY).
CC -1 MISCELLANEOUS: PURIFIED 65 kDa ANTIGEN CAN ELICIT A STRONG DELAYED-TYPE HYPERSENSITIVITY REACTION IN EXPERIMENTAL ANIMALS INFECTED WITH M.TUBERCULOSIS. THIS PROTEIN IS ONE OF THE MAJOR IMMUNOREACTIVE PROTEINS OF THE MYCOBACTERIA. THIS ANTIGEN CONTAINS EPITOPES THAT ARE COMMON TO VARIOUS SPECIES OF MYCOBACTERIA.
CC -1 SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).
CC -----
DR EMBL; M15467; AAA8232.1; -.
DR EMBL; AL021932; CAI17397.1; -.
DR EMBL; AE006948; AAK44679.1; -.
DR EMBL; M17705; AAA25358.1; -.
DR EMBL; U55833; AAC44451.1; -.
DR EMBL; U55825; AAC44458.1; -.
DR EMBL; U17825; AAB39044.1; -.
DR EMBL; U17957; AAB39076.1; -.
DR EMBL; S76635; -. NOT_ANNOTATED_CDS.
DR PIR; A26950; A26950.
DR PIR; A43509; A43509.
DR HSSP; PA5746; 1SRV.
DR TIGR; MT0456; -.
DR Tuberculist; RV0440; -.
DR InterPro; IPR001844; Chaperonins_cpn60.
DR InterPro; IPR002423; TCPI_cpn60.
DR Pfam; PF00118; cpn60.rcp1.1.
DR PRINTS; PR00298; CHAPERONIN60.
DR PRINTS; PR00304; TCOMPLEXTCPI.
DR PROSITE; PS00296; CHAPERONINS_CPN60; 1.
KW Chaperone; ATP-binding; Multigene family; Antigen; Cell wall;
KW Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
SQ SEQUENCE 539 AA; 56595 MW; FF03460BAA2C557 CNC64;
Query Match 100.0%; Score 87; DB 1; Length 539;
Best Local Similarity 100.0%; Pred. No. 3;7e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 VLEKKKGAPTTNDG 16
DB 36 VLEKKKGAPTTNDG 51
RESULT 3
CH62_STRAL
ID CH62_STRAL STANDARD: PRT: 539 AA.
AC Q00768;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 60 kDa chaperonin 2 (Protein Cpn60 2) (groEL protein 2) (HSP56).
GN GROEL2 OR GROEL2.

```

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 18.0741 Seconds
(without alignments)
153.143 Million cell updates/sec

Title: US-09-847-637B-3

Perfect score: 87

Sequence: 1 VVLEKKMGAPITNDG 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	59	2	Q9EMD1
2	87	100.0	61	2	Q9EUR7
3	87	100.0	539	2	P97086
4	87	100.0	540	2	Q9AFAS
5	87	100.0	541	2	Q9AGW1
6	87	100.0	541	2	Q9AFAS
7	87	100.0	541	2	Q9KXU5
8	87	100.0	541	2	Q9AFAS
9	87	100.0	541	2	Q9AFAS
10	82	94.3	533	2	Q9FDS2
11	82	94.3	544	2	Q9K2U4
12	77	88.5	538	2	Q9E2V1
13	70	80.5	537	2	Q9K171
14	70	80.5	541	2	Q9K157
15	69	79.3	537	2	Q9JMT6
16	69	79.3	538	2	Q9EY76

17	69	79.3	582	2	Q9REU4	Q9REU4 bifidobacte
18	68	78.2	539	2	Q9RC20	Q9RC20 bacillus sp
19	68	78.2	539	2	Q9E2V4	Q9E2V4 bacillus st
20	68	78.2	542	2	Q9AGE6	Q9AGE6 listeria mo
21	67	77.0	540	2	Q9XCA9	Q9XCA9 rhodothermu
22	67	77.0	540	2	Q9XCA9	Q9XCA9 rhodothermu
23	67	77.0	543	2	Q9AMJ8	Q9AMJ8 anabaena sp
24	67	77.0	543	2	Q9AMJ8	Q9AMJ8 anabaena sp
25	66	75.9	352	2	Q9X2U7	Q9X2U7 oscillatori
26	66	75.9	352	2	Q9X2U7	Q9X2U7 oscillatori
27	66	75.9	546	2	Q9RM09	Q9RM09 leprospira
28	64	73.6	535	2	Q9JGT6	Q9JGT6 tetragenoco
29	64	73.6	540	2	Q9KKF0	Q9KKF0 clostridium
30	64	73.6	540	2	Q9K1V7	Q9K1V7 clostridium
31	64	73.6	542	2	Q9AEP7	Q9AEP7 lactococcus
32	64	73.6	544	2	Q9X6V3	Q9X6V3 bacteroides
33	63	72.4	82	2	Q9F4E5	Q9F4E5 buchnera ap
34	63	72.4	329	2	Q9ETC4	Q9ETC4 serralia ma
35	63	72.4	329	2	Q9EMB0	Q9EMB0 serralia ma
36	63	72.4	329	2	Q9EMW9	Q9EMW9 serralia ma
37	63	72.4	329	2	Q9EMW9	Q9EMW9 serralia ma
38	63	72.4	329	2	Q9F2H2	Q9F2H2 serralia ma
39	63	72.4	329	2	Q9EXM7	Q9EXM7 enterobacte
40	63	72.4	329	2	Q9EXM7	Q9EXM7 enterobacte
41	63	72.4	329	2	Q9EXM5	Q9EXM5 enterobacte
42	63	72.4	540	2	Q9X4R5	Q9X4R5 streptococ
43	63	72.4	540	16	Q97NV4	Q97NV4 streptococ
44	63	72.4	541	2	Q9JEB6	Q9JEB6 enterococc
45	63	72.4	544	16	Q9KNR7	Q9KNR7 vibrio chol

ALIGNMENTS

RESULT 1	ID	Q9EMD1	PRELIMINARY:	PRT:	59 AA.
AC	Q9EMD1	01-MAR-2001 (TREMREL. 16, last sequence update)			
DT	01-MAR-2001 (TREMREL. 16, last sequence update)				
DE	01-DEC-2001 (TREMREL. 19, last annotation update)				
HEAT-SHOCK PROTEIN (FRAGMENT).					
GROEL2.					
GN	Streptomyces coelicolor.				
OC	Bacteria: Firmicutes: Actinobacteria: Actinobacteridae:				
OC	Actinomycetales: Streptomycineae: Streptomycetaceae: Streptomyces.				
OX	NCBI_TaxID=1902;				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-1802:				
RA	Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;				
RT	"A cold-shock-like gene with pleiotropic effects on Streptomyces				
RT	antibiotic biosynthesis."				
RL	Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.				
DR	EMBL: AJ250536; CAC19351.1; -				
DR	HSSP: P06139; IAO.				
DR	InterPro: IPR002423; TCPI_cpn60.				
DR	Pfam: PF00118; cpn60_TCP1_1.				
DR	PRINTS: PR00304; TCOMPLEXTCP1.				
FT	ATP-binding; Chaperone.				
FT	NON_TER				
SO	SEQUENCE	59 AA; 6407 MW; E7B2419B7DE68FA CRC64;			
QY	1 VVLEKKMGAPITNDG 16	100.0%; Score 87; DB 2; Length 59;			
DB	37 VVLEKKMGAPITNDG 52	Best Local Similarity 100.0%; Pred. No. 2.4e-07;			
		Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
RESULT 2					

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O9EUR7
ID Q9EUR7 PRELIMINARY: PRT; 61 AA.
AC Q9EUR7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HEAT-SHOCK PROTEIN (FRAGMENT).
GN GROEL2.
OS Streptomyces hygroscopicus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF 141;
RA Martinez-Costa O.H., Zalacain M., Alkema W., Holmes D., Malpartida F.;
RT "A cold-shock-like gene with pleiotropic effects on Streptomyces
RT antibiotic biosynthesis."
P EMBL; AJ250537; CAC19355.1; -.
DR HSSP; P06139; 1AON.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00304; TCOMPLEXTCP1.
KW ATP-binding; Chaperone.
FT NON_TER 61
SQ SEQUENCE 61 AA; 6645 MW; D20095FA199B7CA CRC64;

Query Match 100.0%; Score 87; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 2.5e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 3
P97086 PRELIMINARY: PRT; 539 AA.
AC P97086;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella tyrosinosolvens.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=57704;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IMTB D-1411;
RA Zimmermann O., Pinkenburg O., Koechel H.G.;
RT "Tsukamurella tyrosinosolvens sp. nov. hsp60 gene for heat shock
RT protein 60."
P Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DE EMBL; U90204; AAB49990.1; -.
DR HSSP; P06139; 1GRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 539 AA; 56137 MW; 6335314830C9B662 CRC64;

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Query Match 100.0%; Score 87; DB 2; Length 539;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 4
O9AFAS PRELIMINARY: PRT; 540 AA.
AC O9AFAS;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN).
GN HSP60.
OS Tsukamurella paurometabola.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriineae; Tsukamurellaceae; Tsukamurella.
OX NCBI_TaxID=2061;
RN [1]
RP SEQUENCE FROM N.A.
RA Zimmermann O.S., Koechel H.G.;
RT "Tsukamurella paurometabola heat shock protein 60 (hsp60) gene."
P Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND
CC PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS
CC CONDITIONS (BY SIMILARITY).
CC -!- SUBUNIT: OLIGOMER OF 14 SUBUNITS COMPOSED OF TWO STACKED RINGS OF
CC 7 SUBUNITS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DE EMBL; AF352578; AAK18614.1; -.
DR HSSP; P06139; 1GRU.
DR InterPro: IPR001844; Chaperonins_cpn60.
DR InterPro: IPR002423; TCPL_cpn60.
DR Pfam: PF00118; cpn60_TCPL_1.
DR PRINTS: PR00298; CHAPERONIN60.
DR PRINTS: PR00304; TCOMPLEXTCP1.
DR PROSITE: PS00296; CHAPERONINS_CPN60; 1.
KW ATP-binding; Chaperone.
SQ SEQUENCE 540 AA; 56506 MW; 524E5CDB2C49BF7C CRC64;

Query Match 100.0%; Score 87; DB 2; Length 540;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLEKKKGAPTITNDG 16
DB 37 VLEKKKGAPTITNDG 52

RESULT 5
O9KGW1 PRELIMINARY: PRT; 541 AA.
AC O9KGW1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
OS Mycobacterium avium.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacteriineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1764;
RN [1]
RP SEQUENCE FROM N.A.
RA Nagabushanam V., Praszkier J., Cheers C.;
RT "Molecular and immunological characterization of the M. avium homolog
RT of Hsp65."
P Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PREVENTS MISFOLDING AND PROMOTES THE REFOLDING AND

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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:25:57 ; Search time 22.5185 Seconds
(without alignments)
78.921 Million cell updates/sec

Title: US-09-847-637B-3
Perfect score: 87
Sequence: 1 VLEKKWGAPITINDG 16

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
1 number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A_Geneseq_Q32802:*
2: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
3: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
4: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
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14: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1992.DAT:*
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18: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1996.DAT:*
19: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:*
20: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
21: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	16	21	AAV93330
2	87	100.0	22	21	AAV93328
3	87	100.0	215	19	AAW60145
4	87	100.0	215	20	AAV14892
5	87	100.0	295	22	AAAB31615
6	87	100.0	523	19	AAW60144
7	87	100.0	523	20	AAV14891
8	87	100.0	539	20	AAV23919
9	87	100.0	540	9	AAW81351
10	87	100.0	540	16	AAW81610
11	87	100.0	540	18	AAW32100

12	87	100.0	540	19	AAW44702
13	87	100.0	540	20	AAV23911
14	87	100.0	540	21	AAV93332
15	87	100.0	540	22	AAE11755
16	87	100.0	540	22	AAW81118
17	87	100.0	540	22	AAAB31606
18	87	100.0	541	16	AAW67384
19	87	100.0	541	20	AAV14909
20	87	100.0	541	20	AAV23910
21	87	100.0	541	20	AAV23913
22	87	100.0	544	18	AAW32099
23	87	100.0	560	9	AAW80215
24	87	100.0	572	11	AAW04716
25	87	100.0	573	11	AAW04715
26	87	100.0	573	16	AAW64765
27	87	100.0	573	16	AAW64766
28	87	100.0	588	9	AAW80364
29	87	100.0	638	21	AAW03790
30	87	100.0	639	22	AAW31609
31	87	100.0	648	22	AAW31614
32	87	100.0	948	22	AAW31611
33	84	96.6	95	22	AAU04567
34	82	94.3	612	22	AAU63908
35	81	93.1	16	18	AAW43458
36	81	93.1	548	17	AAW94368
37	81	93.1	548	22	AAW92732
38	76	87.4	16	17	AAW94780
39	72	82.8	440	13	AAW22363
40	72	82.8	540	13	AAW22363
41	70	80.5	15	18	AAW43459
42	68	78.2	52	13	AAW20195
43	68	75.9	544	20	AAV23905
44	66	75.9	545	20	AAV23930
45	66	75.9	547	16	AAW67381

ALIGNMENTS

RESULT 1
AAV93330
ID AAV93330 standard; peptide: 16 AA.
XX
AC AAV93330:
XX
DT 04-SEP-2000 (first entry)
XX
DE Amino acid sequence of an epitope of heat shock protein 60.
XX
KW Epitope: heat shock protein 60; Hep60; vaccine; autoimmune disease;
KM Inflammatory disorder; arthritis.
XX
OS Mycobacterium tuberculosis.
XX
PN W0200027870-A1.
XX
PD 18-MAY-2000.
XX
PF 04-NOV-1999; 99W0-IL00595.
XX
PR 05-NOV-1998; 98US-0107213.
XX
PA (HADA-) HADAST MEDICAL RES SERVICES & DEV.
XX
PI Naparstek Y, Ulmansky R, Kashl Y;
XX
DR WPI: 2000-376486/32.
XX
PT Peptide having a defined sequence is used in vaccines for conferring
PT Immunity against autoimmune disease or inflammatory disorders,
XX especially arthritis -
XX
PS Claim 3; Page 7; 58pp; English.

XX The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.

XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 87; DB 21; Length 16;

Best Local Similarity 100.0%; Pred. No. 2.8e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKWGAPTITNDG 16

DB 1 VVLEKKWGAPTITNDG 16

XX
 ID AAY93328 standard; peptide: 22 AA.

XX
 AC AAY93328;

XX
 DT 04-SEP-2000 (first entry)

XX
 DE Amino acid sequence of an epitope of heat shock protein 60.

XX
 KM Epitope: heat shock protein 60; Hsp60; vaccine; autoimmune disease;

XX
 KM Inflammatory disorder; arthritis.

XX
 OS Mycobacterium tuberculosis.

XX
 PN W0200027870-A1.

XX
 PD 18-MAY-2000.

XX
 PF 04-NOV-1999; 99WO-IL00595.

XX
 PR 05-NOV-1998; 98US-0107213.

XX
 PA (HADA-) HADASIT MEDICAL RES SERVICES & DEV.

XX
 PI Naparstek Y, Ulmansky R, Kashi Y;

XX
 DR WPI: 2000-376486/32.

XX
 PT Peptide having a defined sequence is used in vaccines for conferring
 PT immunity against autoimmune disease or inflammatory disorders,
 PT especially arthritis -

XX
 PS Claim 1; Page 7; 58pp; English.

XX
 CC The present sequence represents an epitope of the heat shock protein
 CC 60 (Hsp60) of Mycobacterium tuberculosis. The peptide, and the
 CC nucleic acid encoding it, are useful in vaccines for conferring
 CC immunity against autoimmune disease or inflammatory disorders,
 CC especially arthritis. The peptide may also be used to raise
 CC antibodies, which are then used for passive immunisation.

XX
 SQ Sequence 22 AA;

Query Match 100.0%; Score 87; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 4.1e-08; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKWGAPTITNDG 16

DB 7 VVLEKKWGAPTITNDG 22

RESULT 3

AAW60145
 ID AAW60145 standard; Protein: 215 AA.

XX
 AC AAW60145;

XX
 DT 25-AUG-1998 (first entry)

XX
 DE M. vaccae antigen GV-27A sequence.

XX
 KM Mycobacterium vaccae; antigen; therapy; prevention; cytokine production;
 KM M. avium; M. tuberculosis; immune response enhancer; cell proliferation;
 KM mycobacteria infection; vaccine; cancer.

XX
 OS Mycobacterium vaccae.

XX
 PN W09808542-A2.

XX
 PD 05-MAR-1998.

XX
 PF 28-AUG-1997; 97WO-N200105.

XX
 PR 12-JUN-1997; 97US-0873970.

XX
 PR 29-AUG-1996; 96US-0705347.

XX
 PA (GENE-) GENESIS RES & DEV CORP.

XX
 PI HiYama J, Prestidge RL, Scott LM, Skinner MA, Tan P;

XX
 PI Visser E;

XX
 DR WPI: 1998-216926/19.

XX
 DR N-PSDB; AAV34609.

XX
 PT Mycobacterium vaccae polypeptides - used to develop products for use
 PT in detection, therapy and prevention of mycobacteria infections or
 PT as immune response enhancers

XX
 PS Claim 48; Pages 117-118; 153pp; English.

XX
 CC This represents a Mycobacterium vaccae antigen GV-27A. The invention
 CC provides M. vaccae polypeptides that comprise an immunogenic portion of
 CC a soluble M. vaccae antigen, or a variant, where the antigen induces an
 CC immune response in patients previously exposed to a mycobacterium. Such
 CC M. vaccae polypeptides can be used in methods for enhancing non-specific
 CC immune response. The methods and products can be used for the detection,
 CC treatment and prevention of infectious diseases caused by mycobacteria
 CC such as M. vaccae, M. avium or M. tuberculosis. The products also have
 CC the ability to induce cell proliferation and cytokine production (e.g.
 CC interferon-gamma and interleukin-12 production) in T cells, NK cells,
 CC B cells, or macrophages. They can be used for enhancing immune responses
 CC for use in vaccines or immunotherapy of infectious diseases and cancers.

XX
 SQ Sequence 215 AA;

Query Match 100.0%; Score 87; DB 19; Length 215;

Best Local Similarity 100.0%; Pred. No. 6e-07; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVLEKKWGAPTITNDG 16

DB 37 VVLEKKWGAPTITNDG 52

RESULT 4

AAV14892
 ID AAV14892 standard; protein: 215 AA.

XX
 AC AAV14892;

XX
 DT 25-OCT-1999 (first entry)

XX
 DE Amino acid sequence of M. vaccae antigen GV-27A.

XX
 KM Mycobacterium vaccae protein; antigen; T cell activation; cytokine;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 17, 2002, 17:26:02 : Search time 9.48148 Seconds
(without alignments)
41.218 Million cell updates/sec

Title: US-09-847-637B-3
Perfect score: 87
Sequence: 1 VVLEKKMGAPITINDG 16

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Issued Patents-AA:*

1: /cgn2_6/ptodata/1/laa/5A.COMB.pep:*
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4: /cgn2_6/ptodata/1/laa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/laa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/laa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	87	100.0	215	2	US-08-997-080-117 Sequence 117, App
2	87	100.0	215	2	US-08-997-362-117 Sequence 117, App
3	87	100.0	215	4	US-09-095-855-117 Sequence 117, App
4	87	100.0	215	4	US-09-324-542-117 Sequence 117, App
5	87	100.0	523	2	US-08-997-080-114 Sequence 114, App
6	87	100.0	523	2	US-08-997-362-114 Sequence 114, App
7	87	100.0	523	4	US-09-095-855-114 Sequence 114, App
8	87	100.0	523	4	US-09-324-542-114 Sequence 114, App
9	87	100.0	540	2	US-08-368-834-20 Sequence 20, Appl
10	87	100.0	540	4	US-08-461-722-3 Sequence 3, Appl
11	87	100.0	540	4	US-08-461-722-4 Sequence 4, Appl
12	87	100.0	540	4	US-08-336-251-3 Sequence 3, Appl
13	87	100.0	540	4	US-08-336-251-4 Sequence 4, Appl
14	87	100.0	540	5	PCT-US94-06362-3 Sequence 3, Appl
15	87	100.0	540	5	PCT-US94-06362-4 Sequence 4, Appl
16	87	100.0	541	2	US-08-467-822-34 Sequence 34, Appl
17	87	100.0	541	2	US-08-447-154-19 Sequence 19, Appl
18	87	100.0	541	2	US-08-997-080-160 Sequence 160, App
19	87	100.0	541	2	US-08-997-362-160 Sequence 160, App
20	87	100.0	541	2	US-09-095-855-160 Sequence 160, App
21	87	100.0	541	4	US-08-432-697-34 Sequence 34, Appl
22	87	100.0	541	4	US-08-466-248-34 Sequence 34, Appl
23	87	100.0	541	4	US-09-324-542-160 Sequence 160, App
24	66	75.9	548	2	US-08-467-822-31 Sequence 31, Appl
25	66	75.9	548	4	US-08-432-697-31 Sequence 31, Appl
26	66	75.9	548	4	US-08-466-248-31 Sequence 31, Appl
27	63	72.4	547	4	US-08-461-722-2 Sequence 2, Appl

28	63	72.4	547	4	US-08-336-251-2	Sequence 2, Appl
29	63	72.4	547	5	PCT-US94-06362-2	Sequence 2, Appl
30	63	72.4	548	2	US-08-467-822-32	Sequence 32, Appl
31	63	72.4	548	4	US-09-472-971-3	Sequence 3, Appl
32	63	72.4	548	4	US-08-432-697-32	Sequence 32, Appl
33	63	72.4	548	4	US-08-466-248-32	Sequence 32, Appl
34	59	67.8	547	2	US-08-467-822-35	Sequence 35, Appl
35	59	67.8	547	4	US-08-432-697-35	Sequence 35, Appl
36	59	67.8	547	4	US-08-466-248-35	Sequence 35, Appl
37	59	67.8	573	4	US-08-461-722-1	Sequence 1, Appl
38	59	67.8	573	4	US-08-336-251-1	Sequence 1, Appl
39	59	67.8	573	5	PCT-US94-06362-1	Sequence 1, Appl
40	57	65.5	573	2	US-08-706-209-1	Sequence 1, Appl
41	57	65.5	573	3	US-08-981-787-1	Sequence 1, Appl
42	57	65.5	573	5	PCT-US96-11373-1	Sequence 1, Appl
43	57	65.5	573	5	PCT-US96-11375-1	Sequence 1, Appl
44	55	63.2	545	2	US-08-467-822-30	Sequence 30, Appl
45	55	63.2	545	4	US-08-432-697-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-08-997-080-117
Sequence 117, Application US/08997080
Patent No. 5968524
GENERAL INFORMATION:
APPLICANT: WATSON, JAMES D.
APPLICANT: TAN, PAUL L.J.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
NUMBER OF SEQUENCES: 194
CORRESPONDENCE ADDRESS:
ADDRESS: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASTESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 215 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-997-080-117
Query Match 100.0%, Score 87, DB 2, Length 215:
Best Local Similarity 100.0%, Pred. No. 2e-07:
Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0:
QY 1 VVLEKKMGAPITINDG 16

Db 37 VLEKKWGAPTITNDG 52

RESULT 2

US-08-997-362-117

Sequence 117, Application US/08997362

Patent No. 5985287

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Hiyaama, Jun

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Scott, Linda

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR

TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS

NUMBER OF SEQUENCES: 194

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/997,362

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970

FILING DATE: June 12, 1997

APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347

FILING DATE: August 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-997-362-117

Query Match 100.0%; Score 87; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKWGAPTITNDG 16

Db 37 VLEKKWGAPTITNDG 52

RESULT 3

US-09-095-855-117

Sequence 117, Application US/09095855

Patent No. 6160093

GENERAL INFORMATION:

APPLICANT: Tan, Paul

APPLICANT: Visser, Elizabeth

APPLICANT: Skinner, Margot

APPLICANT: Prestidge, Ross

TITLE OF INVENTION: Compounds and Methods for

TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections

NUMBER OF SEQUENCES: 208

CORRESPONDENCE ADDRESS:

ADDRESSEE: Law Offices of Ann W. Speckman

STREET: 2601 Elliott Avenue, Suite 4185

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98121

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/095,855

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/705,347

FILING DATE: 23-AUG-1996

APPLICATION NUMBER: 08/873,970

FILING DATE: 12-JUN-1997

APPLICATION NUMBER: 08/997,362

FILING DATE: 23-DEC-1997

ATTORNEY/AGENT INFORMATION:

NAME: Sleath, Janet

REGISTRATION NUMBER: 37,007

REFERENCE/DOCKET NUMBER: 11000.1002c3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-269-0565

TELEFAX: 206-269-0563

TELEX:

INFORMATION FOR SEQ ID NO: 117:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-095-855-117

Query Match 100.0%; Score 87; DB 4; Length 215;

Best Local Similarity 100.0%; Pred. No. 2e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLEKKWGAPTITNDG 16

Db 37 VLEKKWGAPTITNDG 52

RESULT 4

US-09-324-542-117

Sequence 117, Application US/09324542

Patent No. 6328978

GENERAL INFORMATION:

APPLICANT: Watson, James D.

APPLICANT: Tan, Paul L.J.

APPLICANT: Ross

TITLE OF INVENTION: Methods and Compounds for the Treatment

TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders

FILE REFERENCE: 11000.1007c1

CURRENT APPLICATION NUMBER: US/09/324,542

EARLIER FILING DATE: 1999-06-02

EARLIER APPLICATION NUMBER: US 08/997,080

NUMBER OF SEQ ID NOS: 194

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO: 117

LENGTH: 215

TYPE: PRT